

81/162

**FIGURE 75**

CGGGTCTGTAGTACCTTACCTGTACGAGTGTGTTAGGATGAGATATGTTTGTGAATCTTAAACATATATAA  
 ACGTGTGCTACTGTGAGARCTGGAACAAAGAAAGAGAGCGGAGTGTGAGAGAAATCAAGGGAGGGCTGGGGCTGGGAA  
 AGRACGAAAAAGCGGATCGGCTATAGAGGAGAGGGGACAGTCTCGGAGGCCACACTTTGCAATGAAGACTTTTAGAC  
 TTTCTGCCGGGAGAGCGGGCCACAGCGCCAGGTCTGTAGUAGGAGGCCCGAGGGGCGGGTCCCTCAGAAAGCCTA  
 CAGGTGAGATATCGGTTCTCCCTTCTCCGCTTCGGTTCGAGAGGAGGGGAGGAGCGTCTCCCTGTTCTGATCCT  
 ATCGGAGGCGGCGCAGGCGCGGCTTGGCCTTCCTGTGGAGCGGGAGGGGGGCGGATGTGTCAACCAATACCA  
 GTGGGAGCGGTCTGGTGTGGACCAAGCGCGGCGAGGTCTGGGTAGAGTATAAGAGCTCGAGGGAGCGGGCGGGGCG  
 CAGACGCTCGAGAACATCTCCAGACGTCGAGAGCCCGAGGCGGAGAGTCTCCGCGCTCATCTCGGCGCGCTC  
 GGTCCGCGTCTCTCTCCGCGCACATAGGCTCGGGGCCCCGGCTCTCGCGCGCGCTCAAGCGCTCGGCTCGGCTGTCTG  
 CTGCTGGTGTCTGGGGGAGTGTCCCGGCGCACAGGCGCGCGCAGGACCACTGCACGTGTCCCAACCAAGATGAC  
 GGTGTGCGAGCCCGAGCGGCCCCGGGCGGCGCTGCCAGTGGCGCGCTGGGCTCGGGCATGGGGCTGCACTGCT  
 CCACGCTGACCTCCAAAGTGTCTCTGCTCAAGGGCGGCGCATGAGCGGCCCCCAAGAACGCCCGACGCTGGTGTGCG  
 CGAGTGAAGCACGCGCTCTGGACACAGATGGGCTCTACGACCGCGACTGCGACCGCGAGGGCGGCTCAAGAGC  
 GCGCCAGTGCACACAGAGCTGCTGTCTGGTGGGTAACTCGGTGGGCGTGGCGCGCGCAGGACAGGGGGGAGCC  
 TGAGCTACAGCTGCGATGAGCTGGTGGCGACCCACCACTCTCTATTGACCTGCGGCCACCGCGCGCGCGCGG  
 GCTTTCACCACTCAGAGCTGGAGCGCGGAGCTGAGCGGCTCTTCGCGAGCGCTATCGGCTGACCGCGCAAGT  
 CGTGGCGCGCTGCTACTAGAGCAGCCCAACCATCCAGATGAGCTGGCGGACAGCACTCTCAGAAAGCGCGCG  
 GTGAAGTGGATATCGGCGATCGCGCTACTACTTCGAGGGGACATCAAGGGGAGTCTCTATTCCAGGGGCGCG  
 GCGGCGCTGAGCTTCTCGCTGGCGGAGAACCTCTGAGGTGGAGCGACCTCATCTATTACCTGGAGCAGAT  
 TCCCGCGAGGTTCTCCATGAAGCGCTCACCGCCGGCTCATCGCGCTCATCTGGTGGTGGTGGCGCTCG  
 TCGCGGCGATGGCGCTCTGGTGTATCACCACCGGAGAAAGTGGGGAGGTACAGAAAGGTGGAGATCAAGGAA  
 CTGGGGGATGTGAGAAAGGAACCGGCTTGTAGGTACCGCGCGGGCGAGGGATGGGTTGGGTACCGGATTTTC  
 GGTATGCTCCAGAGCCAAAGTGAATCAGCTTCTGATCTCTCGCGCAAGAGGAGCTTTATCCCTTTCAAAAT  
 CCTGCTTCCCCCTCTCTTTTGGGACACACCGAGTTTAAATAGATCTGGGCTCAGGGTCTCTTCTCTCA  
 CTCTCTCTTGGGGAGGATTTCTAAATGTATCCCCCTTCGCTCCACACAGGAAACCTGACTGGGGGAGT  
 GAGGAGAGGATGGCACAGCGTTATGTGTATAAAACAAAGTATCTGTATGACACCGGAGCTGTTTCAAGTAA  
 CTGAATCCATCTGGACATTGTGAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGGCTTGGGTTTA  
 AATATTTGATGATCTCCACTTGTATCATGGCTACCGAGGAGAGAGGAGTTGTTAACTGGGCTATGTGTA  
 TAGGCTCATTTACCATCGTTTGTATTAATGACACCATATGCTGTCTACTGGGAAAGAGGCTGTTTCAAGTGGC  
 TGAACGAGTGTGGATGCTTTGAGGACAGACATTGCGCGGAACTCAGTCTATTTATTTCTTCAGCTTGCCCT  
 ACTGCCACTGAGTGTGATGCTTTGAGGACAGACATTGCGCGGAACTCAGTCTATTTATTTCTTCAGCTTGCCCT  
 ATTTTTTAAATAAARACAGAAATTAATAAANTATGGGAAAGGCACAAACAGAGCTCGGCTTTGGAAGAGT  
 CCGCTCGAGTTTCTATCACTTTGGTCTCTAATTTCCCAAGACTTGTATTTTTTTTTTATTTCAAAATTAACAC  
 TTTTTTCCCGGAGAGTGGGTGTTCTATGTTGCTACTGTGGTGTCTCCAGAGATATCTTAATCTAGCGAGTGT  
 AAATGCTATCTTTCTAAATTAAGTTTATTTGGAACCTTCCTTCAAACTGCGAGGAGCGAGCTCTGAGGGCGG  
 AGAGCTAAAN/TAGCTGCTTTTGTGAAAGAGTGGCAGTCTTTGGTCTCTCTAAACAGGCTTCTCACCA  
 ATGGAGACAGAAACTCTAGTTCAAGAGCTGTACTCTCTTGAATCCAGCGCTACTCGAATTAAGTGGTACTA  
 TTTCCATTTAGCTTTTGAACAACTCACTTAACCTCAAGGCGTTTGGCTCTAAGATTAAACGAGCTTT

[illegible]





[illegible]

86/162

**FIGURE 79**

MRAAYLFILFLFAGLLAQGGYDLDPFPFPDBVQYENHSDQIDNFDYYDYQEVTPRPSEEQFQFQSQGGVQQEV  
IPAPTFEPFGHAELEPTEPGFLDCREEQYPCTRLYSIHAPCKQCINEVCFFYSLREVTYVINKELICVRTVCAREELI  
RADLCROKRFKCGVMASGLCQSVASCARSCGSC

Signal sequence.

amino acids 1-19

N-myristoylation sites.

amino acids 161-166, 167-172

87/162

**FIGURE 80**

HAARELPVSPARALLLALAGALLAPCEARGVSLMNEGRADEVVSASVRESGDLWIEPVKSPDSKNHFEVLNLRQR  
 ESKELIINLERNEGLIASSFTTETHYLQDGTIVSLARNYTVILGHCIYHGHVRCYSOSAVSLSTCSGLRGLYVFE  
 NESXYVLEPMKSATNRYKLFFPAKKLKSVRGSCGSHRNTFNLAARKNVFFPPSQWAPRRKRRETKATRYVELVIVA  
 DNKEFQRQKDLKRYKQRLLETIANHFVDKFYRPLNTRIVLVGVEVNDMDKCSVQDPFTSLHEFLDWRKQKLLP  
 RKSHDNAQLVSGVYFQGTITIGNAPIMQMTADQSGGIYMDHSHNELGAAVTLAHELGHNFQGMHDTLDPCCSCQ  
 NAVEKGGCINNASTGYFFPMVFSKSCSKDLETSLEKMGVCLFNLPEVRESFGGQKCGNRFVEEGECCDCGSE  
 EOMNRCCNATCTLEKPAVCAHGLCCEDCQLKPACTACKDSSNSCDLPEFCTGASPHCFANVYLDHGHSCQDVD  
 GYCYNIGICQTHGQCQVTLNMGPAKPAFGICFERVINSAGDEYGNCKVSKSSFAKCEMRDAKCGKIQCCGASRP  
 VIGTHAVSTETNIPLQQGGRILCRGTHVYLQDDMPDPGLVLGATKCADGKICLNPQCQNHISVFGVHECAMQCHG  
 RGVCMNRKNCRCERWAPFPCKDFGFGESTDSGYIROADNQGLTIGILVTTICLLAAGFVVYLKAKTLIRLLPT  
 NKKTTILEMLRCVRPSEKPRGFPQCOAHGLHGLKGLMRKFPDSYPPKDNPRRLQCCVNDISREPLAGLIVPQPS  
 TQEVLPPLHAKAPRAPSVFANPLAKPALRQAQGTCKPNPPQKPLPADPLARTTRLEHALAPFFGQWETGLRLAP  
 LRPAQYXPHQVPRSTHTAYIK

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 709-729

**N-glycosylation sites.**

amino acids 111-114, 149-152, 381-384, 452-455, 651-654

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 206-209, 730-733, 742-745

**N-myristoylation sites.**amino acids 89-93, 103-108, 177-182, 180-185, 313-318, 343-348, 377-382,  
 407-412, 423-428, 424-429, 524-529, 630-635, 635-640, 656-661, 668-673,  
 694-699, 708-713, 712-717, 878-883**Neutral zinc metalloproteases, zinc-binding region signature.**

amino acids 347-356

**Disintegrins proteins.**

amino acids 454-504, 410-460, 486-536

88/162

**FIGURE 81**

MASRSMRLLELLSCLAKFGVLESDIIMEPSCAPGWFTKSNICYGYFRKLRRNSDAELECCQSYGNCAHLASILSLK  
EASTIAEYISGYQRSQPIWIGLHDPQKRQQNQNTQGAMLYR3WSSGKSMGGNKHCAETSSNNNPLTWSSNECNK  
RQHFTCKYRP

Signal sequence.

amino acids 1-22

N-glycosylation site.

amino acids 50-53

N-myristoylation sites.

amino acids 64-69, 125-130

C-type lectin domain signature.

amino acids 129-154

Lectin C-type domain.

amino acids 47-156



89/162

**FIGURE 82**

MATMENKVICALPLVSNLALGTLAAQTETCTFVAERERQNCGFFGVTPSQCANRGGCCFDUTVRGVVPCFYENTL  
DVFEDEECDF

Signal sequence.

amino acids 1-24

N-myristoylation sites.

amino acids 45-50, 64-69

Trefoil (P-type) domain.

amino acids 30-71

90/162

**FIGURE 83**

MLFQIFPLLLVSLNIVRGVFFYAEKYQTFTGIGGLENTKTKTQTFPIFYTIKSKGLAVRGSGSTEGFPFGASPRGHP  
 GFSGGFPKPGYSSPGLQGEPLPGFPQPSAVGKPGVPGLEKPGGERCFYSPKGDVGPAGLPGPRGFPFPFPIPG  
 PAGISVPGRPGQGGPTGAPGPRGTFEGEKGAPGVPGMIGQKGEKGYGAPGKPOERGLPGFQGGTGPSGFPFGVGR  
 GENGVPQGPGKLGDRGFFGEMGFIGFPQGPQGPGERGPEGIGRFGAAGAPGQPGILPGTKSLPGAFGLGFPFGFP  
 GFGKPLPLGLKGERGFPAGLPGGPGAKGEGQGPAGLPKPKPLTGFPFGMGPQGPFGKIPGSHGLPGPKGTGFAQFA  
 GYFGAKGERGSPGSDGREGYFGKPLDGGPKGNPGLPGPKKDPGVGGFPGLPGFVGPAGAKGMPGHNGEAGPPGA  
 PGTPTRGPIGGPPIGFTGSKGDPGSPGPPGAGIATKGLNGPTGPPGFPFGPRGPGSGEGLEGFPFGPPGPGQ  
 AVNFEGLKAGQRGLSGTPLVBAKQGVTCMPVSAFTVILSKAYPAIGTPIEFKILYNRQQHYDPRFTGLFTCQ  
 IPGLIYFYSYHVRVKGTHVWVGLYKNGTFVMTYDVTYKSYLDQAGGSAIIDLTTENDQVNLQLFNABSNGLYSSSE  
 YVHSSTSGFLVAFM

**Signal sequence.**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 116-123

**N-myristoylation sites.**

amino acids 18-23, 276-281, 317-322, 350-355, 380-385, 415-420, 446-451,  
 529-534, 548-553, 587-592, 613-618, 661-666

**Amidation site.**

amino acids 219-222

**Clq domain signature.**

amino acids 571-601

**Clq domain.**

amino acids 553-677

**Collagen triple helix repeat (20 copies).**

amino acids 92-159, 156-214, 223-281, 282-340, 344-403, 404-463, 466-522

91/162

**FIGURE 84**

NPLPPLL LLL LLAAPWGSAVPCVSGGLPKFANITFLSINMKNVLCWTPPEGLQGVKVTYTVQYFTYGGKWLKNS  
ECRNINATYCDLSAETS DYENQYYAKVKAINGTKCSKWAHSGRIYFPFLETQIGPFEVALTTDEKSI SVVLTAPE  
KWKRNPEDELFVSMQQIYSNLEKYNVSVLNTKSNRTWSQCVTNRTDLVLTWLEPNTLYQVHVESFVPGPPRAQPSR  
KQCAKTLKQSSSEPKAKILFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHVAMLYILIYGNFQKRFFVPAEKI  
VINFTLTNTSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLAPFQSEEEVVKHLGYASHIMEIFCDSEENTEGTS  
LTQQESLGRTIPPDKTIVIEYDYVRTIDICAGPEEQELSLQEEVSTQCTLLESQAALAVLGPQTLQYSYTPQLQ  
DLDP LAGENTDSEEPPEEPFSTTLVQNDPQTGRICIPSLSSFDQDSEGCZFSEGDGLGEEGLLSRLYEFPAPDR  
PFGGNETYIMQFMEEWGLYQNNEN

**Signal sequence.**

amino acids 1-18

**Transmembrane domain.**

amino acids 239-259

**N-glycosylation sites.**

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192, 304-307, 523-526

**Tyrosine kinase phosphorylation sites.**

amino acids 385-392, 518-526

**N-myristoylation sites.**

amino acids 53-58, 106-111, 368-373, 492-497

**Phosphatidylinositol 3- and 4-kinases proteins.**

amino acids 253-279

**Tissue factor.**

amino acids 1-278

92/162

**FIGURE 85**

MRAPGRPALREPLPLPPELLLLLLAAPWGRAVFCVSGGLPKPANITFFLSINMKRVLQWTFPEGLQGVKVTYTVQYF  
LYGQKKWLKKSECRNINRTYCDLSASTSOYENQTYAKVKAIWGTCKSKMAESGRFYFFLETQIGFPPEVALITDE  
KGISVVLTAPEKWKRNPEELPVSQQIYSAKYNVSVLNTKSNRTWSQCVTNETLVLTWLEPATILYCVNVESFV  
EGPPRRAPQPSERQCARLTKDQSSSEFKAKIIPWYVLPISITVFLPSVMGYSIYRYIHVGEKKRPANLILYGNF  
DKRFFVPAAEKIVINFITLNLSDSKTSHQMSLLGKSSDVSSLNDPQPSGNLRPFQEEELVKLQYASHIMELF  
CDSEENTEGTSLTQQESLSRTIPFDKTVLIEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQ  
TLQYSYTFQLQULDFLAQENTDSEEGPSEEPSTTLVDWDFQTGRLCIFSLSSFDQDSGEGEPSEGDGLGEGLL  
SRLYSEAPDRPPGHEITYLMQFMEWGLYVQMEN

Signal sequence.

amino acids 1-29

Transmembrane domain.

amino acids 240-270

93/162

**FIGURE 86**

MAAARLCGLSLLLSITCVALLLQPLLGAQGAPLEFVYFGDNATPEQMAQYANDLRRIIMLTERPRYCKRKESDTL  
AFSEWGGSPHAAVERELSLDL

Signal sequence.

amino acids 1-29

N-myristoylation site.

amino acids 80-85

Amidation site.

amino acids 65-66

Pancreatic hormone family signature.

amino acids 49-65

Pancreatic hormone peptide.

amino acids 30-65

94/162

**FIGURE 87**

MGPPSAPECRILHVPKKEVLLTASLLTFWNEPTTAKLTLESTPFNVAEGKEVLLLAHRLPQNRICYGWYKGERVD  
GNSLTIVGYVIGTQQATPGPAYSGRETIYPNASLLIQNVTPQNDYTGFTYLAQVIKSDLVNEEATGQPHVYPELEKPS  
ISNNNSNPVEDKDAVATTCERPVQNTTYLWVWQGSLLPVSPLQLSNGNMTLTLLSVKRNDAGSYRCEIQNPAS  
AKRSDPVTINVLVYGFDPGTISP6KANYRPGENINLSCHAASNPPAQYSGWEINGTFQOSTQELFIFPHITVNNSSG  
YMCQAHSNRAGIARNTFTMITVSGSAEVLCAVATVGITIGVLARVALI

**Signal sequence.**

amino acids 1-34

**Transmembrane domain.**

amino acids 322-342

**N-glycosylation sites.**amino acids 104-107, 111-114, 115-119, 152-155, 173-176, 197-200, 224-227,  
256-259, 274-277, 288-291, 292-295, 309-312**Tyrosine kinase phosphorylation site.**

amino acids 206-213

**N-myristoylation sites.**

amino acids 85-90, 211-216, 295-300, 307-312, 332-337

**Immunoglobulin domain.**

amino acids 160-217, 252-301

95/162

**FIGURE 88**

MELKLVLLCWASIAAALEETLLNTKLETADLKWVTFPQVDGQWEELSGLDEEQHSVRTYEVCVDVQAPGQAHWLR  
 TGVWPRRGAVHYVATLRETMLECLSLPRAGRSCKETTVTFVYVESDAITATALTAMMENPYLKVDTVAAEHLTK  
 KRPGAEATFGKVNVTLRGLGSLKAGFYLA PQDQGACMALLSLHLFYMKCAQLTVNLTRFFETVPRELVVPVAGS  
 CVVDVATPAGFSPSLYCREDGQWAEQPVTCGSCAPGFEEAGNTECRACAQQTFFELSGEGSCQPCPRNSHNT  
 IGSVACQCRVGYFRARTDPRGAPCTTTPPSAPRSVVSRLNGSSILALEWSAPLESQGGREDITYALACRECRPGGSC  
 APCGGDLTFDPCFROLVSPWVYVVGRLRPFDTXTTFVTALNGVSSLATGPFVFEFVNVYTDREVPFVAGDIRVTR  
 SSPFSLSLAMAVPRAPGGAVLDYEVKYHERGAEFGSSVRFKTSSENRAELRGLKRGASYLQVVRAREAGYGF  
 GQEHHSQQLDESEGWRQALAGTAVVGVLVLVIVVAVLCLRKQSNGREAREYSDKRGQYLIGHCTKVYTD  
 FPTYEDPNEAVREFAKETIDSVYVKLEEVIGAGEFGVEVCRGRLKAPGKKESCVALKTLKGGYTERQRREFLSEAS  
 IMQGFEPNIIIRLEGVVTNSHPVMILTEFMENGALDSFLPLNDGQFTVIQLVGMLRGIASGMRYLARMSTVHRD  
 LAARNILVNSNLCKVEDPGLSRFLEENSSDYTTSSLGGRIPINWTAPEATAFKFTSASDAWSYGLVMMEVM  
 SFGERFYWMSNQDVINAIEQDYKLPFPFDCPTSLHQLMLDCNQKDRNARFRFPQVVSALDKMTRNFASLKIVA  
 REINGGASHPLLQGRQPHYSATGVSVEWLRAIKMGRYEESSFAAAGFGSFELVSQTSREULLRIGVTLAGGQKRL  
 ASVQRMKSQAKPPTPGGTGGFAPQY

**Signal sequence.**

amino acids 1-15

**Transmembrane domain.**

amino acids 539-559

**N-glycosylation sites.**

amino acids 203-206, 335-338, 426-429, 768-771

**Glycosaminoglycan attachment site.**

amino acids 280-283

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 554-567, 639-642, 795-798

**Tyrosine kinase phosphorylation sites.**

amino acids 508-515, 508-596, 609-614, 729-736

**N-myristoylation sites.**

amino acids 152-157, 182-187, 264-269, 298-305, 317-322, 374-379, 496-501,  
 681-686, 699-704, 719-724, 723-728, 951-956, 975-980

**Amidation site.**

amino acids 637-640

**Tyrosine protein kinases specific active-site signature.**

amino acids 736-749

96/162

**FIGURE 89**

NAQLFLPLLAALVIAQAFAALADVLEGDSSSEDRAFRVPIAGDAPLQGVLGGLALTIVCHVHYLRPFPSARAVLGS  
 PRVKRTFLSRGREAELVLVARGVRVKNVNEAYRFRVALPAYFASLTQVSLASELRPNDSGIYRCEVQHGISDSSD  
 AVEVKVKGVSFVLYRPGSARYAPSFSGAQERACARIGAHATPEQLYAAVYLGGRQCDAGWLSDDQTVRVYPIQTFR  
 ACYGDMDGFGVGRVKNVGVDDLDLYOVYCYAEDINGELFLGDPPEKLTLEEARAYCQERGAETATGQLYAANDG  
 GLDHCSQWLADQSVRYPIVTPSQRCGGELPGVKTLELFPNQTFGFENKHSRNFVYCFRDSAQPSAIFEASNPAS  
 NPASDGLAEIVTVTETLLELQLFQAFESERGAIVSTPIMEDGGGGSGTPEDEALAFKTLLEPQTQSNVPTG  
 FSEEGKALEEKEKYEDRZKESEEREVEDEALWANPSELSSPGFEASLTPEPAQDEKSLQAPARAVLQFG  
 ASPLFDGSEASRPPRVHGPPTETLPTFRERNLASPSPTLVEAREVGEATGGPELSGVFRGESEETGCSSEGAP  
 SLLPTRAPEGTPELEAPSEIDNSGRTAPAGTSVQAQPVLPDTSASRGGVAVVFRASGDCVPSFCHNGGTCLEEE  
 GVRCLCLPGYGGDLCDVGLFCNFGWDAFOGACYHFSITRRSWEAEATQCRMYGAALLASISTPEEQDFINNYR  
 EYQWIGLNDRTIEGDFLWSDGVPLLYENWNFGQDPSYFLSGENCVMVWHRDQGM9DVPCHYHLSYTCRMGLVS  
 CGPPELFLAQVGRPLRYEVDVLYRCREGLAQRNLPLINQENGRWEAFQISCVPRPARALHFESEDPG  
 RQCRLLGRWKALLIPSSFMPPG

**Signal peptide.**

amino acids 1-15

**N-glycosylation sites.**

amino acids 130-133, 337-340

**Tyrosine kinase phosphorylation sites.**

amino acids 126-135, 451-459

**N-myristoylation sites.**

amino acids 47-52, 50-55, 133-138, 142-147, 174-179, 183-188, 281-286,  
 288-293, 297-302, 324-329, 403-408, 414-419, 415-420, 576-581, 586-591,  
 677-682, 684-689, 720-725, 772-777, 811-816

**EGF-like domain cysteine pattern signature.**

amino acids 670-682

**C-type lectin domain signature.**

amino acids 784-809

**Immunoglobulins and major histocompatibility complex proteins signature.**

amino acids 135-142

**Link domain proteins.**

amino acids 166-216, 264-314

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 655-676



97/162

**FIGURE 90**

MAQLFLPLAALNLAQAPALADVLEGDSSSEDAFRVRIAGDAPIQGVLGALTIICHVHYLRPPPSRAVLGS  
 PRVQHTLSRGREEEVIVARGVRVKVNEAYRFRVALPAYPASLTQVSLALSELAFNDSCGIYRCEVQHGIDSSQ  
 AVEVKVKGVVFLYREGSARYAFSFGAQECACRIGAMHATPEQLYAAVYLGVEQCCAGWLSUQTVRYFIQTPRE  
 ACYGDMDGTFGVKNYGVVDPDLDYDVICYAEDLNUELFLGDPPEKITLSEARAYCQERGAETATGQLYAANDG  
 GLVHCSPGNLADGSRVYFIVTPSQRCGGGLPGVKTLFLFENCTGFPNKHRRFNVCYFRDQAQPSAIPASNFAS  
 NPASDGLERIVTVETLEELQLPQETESUSRGAIYSIFINEDGGGGSSTPEDPAEAPRTLEFETQSMVETP  
 FSEEGKALEEEERYEDEEEKEEEEEEEVEDEALNANPSELSSPGPEASLTETEPAAQESLSQAFARAVLPQ  
 ASPLPDGESRABRPFRVHGPFETLPTPRERNLASPSFSTLVEAREVGEATGGPELGVPRGSESEETGSSECAP  
 SLUPATPAPEGTRLEAPSEDMSGRTAPACTSVQAQPVLPDTASRGGVAVVPASGNSAQGSTALSILLFFPL  
 QLNVT

**Signal sequence.**

amino acids 1-15

**Transmembrane domain.**

amino acids 652-670

**N-glycosylation sites.**

amino acids 130-133, 337-340

**Tyrosine kinase phosphorylation sites.**

amino acids 128-135, 451-459

**N-myristoylation sites.**amino acids 47-52, 50-55, 133-138, 142-147, 174-179, 183-188, 281-286,  
 288-293, 297-302, 324-329, 403-408, 414-419, 415-420, 576-581, 586-591**Immunoglobulins and major histocompatibility complex.**

amino acids 135-141

**Extracellular link domain.**

amino acids 156-251, 257-353

**Immunoglobulin domain.**

amino acids 50-139

98/162

**FIGURE 91**

MAVRQNVIALALALALLVVDREVFPVAGKLPFFSTMETCEHMMVESPTCSQMSNLVCGTDTTNTSCQLCLBR.IKT  
KQDTQIMKUGKC

**Signal sequence.**

amino acids 1-20

**N-myristoylation site.**

amino acids 50-63

**Kazal-type serine protease inhibitor domain.**

amino acids 37-86

99/162

**FIGURE 92**

MAPLCFSPWMLPLYLPAPAGLTVQLLSLLLLLVVPHQRLPFMQEDSPLGGSSGSDPLGEEDLPSEEDSPRE  
 EDPFGEDLPGERDLPGERDLPEVKPKSEUEGSLKLEDLPTVEAPGDQEFQNNARRDKEGDDQSHWRYGGDPP  
 WPRVSPACAGRQSPVDLRPQLAATCPALRPLELLGGLPFLPELRIRNNGRSVQLTLPGLEMALCPGRARYA  
 LQLHLHWGAAGRPFSERTVEGHRFPREIHVVRLSTAFARVDEALGRPGGLAVLAFTLEGGPEENGAYEQLLSKL  
 EEIATEGSRTQVPLUISALLPSDFSRYFRYEGSLTFPCAQGVITVTENQTVMLSAKQLHTLSDTLWGPQDSR  
 LQLNFRATQPIAGRTVEAEFFAGVDSSPRAAEPVQLNSCLAAGDILALVFGLLFRVTSVAFLVQMRQHERQTK  
 GGVSYRPAEVAETGA

**Signal sequence.**

amino acids 1-37

**Transmembrane domain.**

amino acids 409-429

**N-glycosylation site.**

amino acids 346-349

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 440-443

**N-myristoylation sites.**amino acids 50-55, 51-56, 209-214, 236-241, 310-315, 339-344, 421-426,  
442-447**Eukaryotic-type carbonic anhydrases signature.**

amino acids 237-253

**Eukaryotic-type carbonic anhydrase.**

amino acids 141-139

100/162

**FIGURE 93**

MCALQLANSAFAVDLFRQLCEKEPLGNVLFSPICLSTSLSLAQVGAKGDTANELGQVLHFEENVKDVPPGFQTPT  
SDVNLKSSFYSLIKRLIVKSLNLSTEFISSTKREYAKELSTVDFKDLSEETKGQINNSIKDLTDGRFENIL  
ADNSVRDQTKILVVNDAYTVGKMMKFESEETKECPFRVNRKTDIKPVQMMNMEATPCMGNTDSINCKITIELPFQ  
NKHLSMFILLPKDVEDESTGLERIEKQLNSELSQNTNPFSTMANAKVKLSIPKFKVEKMTDFKACLENLGKHL  
FSEDTSPFGMSSETKGVALSNVILKVCLEITEDGGDSIEVFGAKILQMKDELNADHPFETIIRHMTYRNTLITFG  
KFCSP

**Signal sequence.**

amino acids 1-42

**N-glycosylation sites.**

amino acids 99-102, 133-136, 188-191, 361-364

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 173-176

**N-myristoylation sites.**

amino acids 130-135, 207-212, 306-311, 312-317

**Serpin (serine protease inhibitor).**

amino acids 3-375

**Fibrillarin proteins.**

amino acids 150-169

101/162

**FIGURE 94**

MDRHSYIFIWLELCAMAVLLTRGETRCYCDAAHCVATGYMCKSELACFSRLLOPQNSNSPLTHGCLDSL  
STTDICQAKQARNHSGTTIPTLECCHEDMCNYRGLRDVLSPPRGEASGGQGNRYQEDGSPRLITKVGELTSSKEL  
WPRAAVIATVPIAGGLYLVLILMLALRMLSENKRRLQDQRQMLSRILNYSFWGHHSKKGQVAKLDLECMVPPVSGH  
ESCCLTCDKMRQADLSNDKILSLVHWGMNSGRGKLEFV

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 152-172

N-glycosylation site.

amino acids 87-90

Glycosaminoglycan attachment sites.

amino acids 121-124, 252-255

N-myristoylation sites.

amino acids 69-73, 249-254

102/162

**FIGURE 95**

MRRNRNDTLASRTLYSSASRSTDLSESDLVNFTIQANFKKRECVFFTKDSKATENVCKGQYQSQHMEGTQI  
 NQSEKWWYKRPTRKFPFDAGFDIQFETLQGGKKKYIRLSCDTDAEILYELLTOHWHLETNINISVTGGAKNEAL  
 NERNRKKIFSRLLYYIAQSKGAWILTGGETHYGLTKYIGSVVRDMTIGRSSEENIVALGIRANGNVSNRDTLIRDCD  
 AEGYFLAQYIMDDPTTRDFLYILDNNRTHLLLVNNGCRGHPTVEAKLANQLEKRISEKTIQDSHYGGKIPIVCFA  
 QGGGKETLKAINTSIKANKIPCVVVEGSGRIADVITASLVVEVDAPTSAGVAKERILVRFLPRTVSRLESSEETESWIK  
 WLKEITLQCSHLLTVIKMEEAGDEIVSNAISYALYKAPSTSEQDKDNWNGQLKLLLEWNLQDLANDEIPTDRRW  
 ESADLQZVMHTALIKDPKFEVLFLNGLNLRKFLTHDVLTELFNSHFTLVYRNLIQAKNSYNDALLTFVVKL  
 VAMFRRGFRKEDANGRDEMDELHGVSPITRNELQALFLWALLQMKKELSRVINWQTRGCTLAALGASKLLKTL  
 ARVKNDINAAAGSEBELANSEYTRAVELFTECYSSOEIDLAELLYVSCBANGGSNCLELAVENTDQRTAQPGVQ  
 NPLSKQWYGEISGRVTKNKKIILCLFIPLVGCQFVSFRKKPVCKRKLWYVVAFTTSPFVVFWMNVVXYIAFL  
 LLFAYVLLMDPHSVPRPELVLVSLVFLCDEVQRQYVNGVNYTTDLNWMVMDTLGLEYFIAGIVFRLHSSNKS  
 SLXSGRVIFCDDYIIFTLRLIHIFTVSRNLGFTIIMLQRMILDVFEELFLFAVWMVAFGVARQGLRQNEQNR  
 WLFRSVIYEPYLAMFGQVPSVDGTFYDFAHCFTTGNEKPLVELDEHNLPRFFENITIPLYCIYMLSTNILL  
 VHLVAMPGYTVGTQEHNDQVVKFQRYFLVQEYCSRNLNIPFPFIVFAYFMVVKKCECCCKEKNMSEVQCF  
 KNEDNLTLANEGVMKENYLVKINTKANDTSEEMRRBFRLQDLTKINDLGLKLLKBIANKIK

**Transmembrane domains.**

amino acids 681-701, 718-738, 734-754, 757-777, 784-804, 819-839, 853-873,  
 951-971, 995-1015

**N-glycosylation sites.**

amino acids 6-9, 75-78, 247-250, 308-311, 812-815, 925-928, 1041-1044,  
 1063-1066

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 83-86

**Tyrosine kinase phosphorylation sites.**

amino acids 21-27, 219-226, 279-286

**N-myristoylation sites.**

amino acids 71-76, 141-146, 174-179, 209-214, 299-304, 577-582, 643-648,  
 904-909

**Amidation site.**

amino acids 102-105

103/162

**FIGURE 96**

MRRNRNDITLDSRTLYSSASRSTDLVSSESLVNFIQAMFKGREGVFFTRDSKATENVCKGXYAQSSQHMEGTQI  
 NQSEKWHYKKNHKEFTPLAAGDIQFRTLGKRGKYIRLSCDTUAEILYELLTQHWHLETNPLVISTVGGAKNFAL  
 KPPMRKIFCRLLYLAQSGKAWILTGGTHYGLMKYIGEVVRDNTISRSEENIVAIGINAWGMVSNRDTLIKNCQ  
 AEGYFLAQYLMDDFTREPLYTLNNETHALLVDNGCHGRPTVEAKLRNQLEKYISERTIQDSWYGGKIPVCF  
 QGGGKETLKAINTSIKKNLPCVVVSSGQIAMVVIASLVEVEDALTSBAVKEKLVKFLPTVSRLPSEETESNIK  
 WLKELLECCHLLTVIAMBEAGDEIVSNALSYALYKAPSTSEQDKNNWNGQLKLLLEWNLQLDLANDEIFTNDRW  
 ESADLQEVMTALIKORPKFVRLFLENGINLRKFLTRDVLTELEFSTLVYKRLQIAKHSYNDALLTFVVKL  
 VANFRKGRERKEDNGRDEMDELHMOVSPITRAFLQALFIWALLQNKKELSKVWEGTRGCTLAALGASKLLKTL  
 AKVNDINAAAGSEELANBYETRAVELFTECYSSDEDLAEQLLVYSCEANGGSGNCLLAVRATDQREFLAQPGVQ  
 NPLSKQWYQELSRDTEKNWKIILCLFIIFLVGCGFVSFRKKEVDKHKKLLWYVVAFFTSPPFVFSWNVVFIATFL  
 LLFAYVLLMDFHSVPPELVELYSLVFLFCDEVQRWYVNGVNYFTDLNVMVMTLSLEYFIAGIVERLESSNKS  
 SLYAGRVIFCLDYIIFTLRLIHFTVSRNLGPKIIMLQRMIDVFFFLPLFAVWMAFGVARQGILRQNEQRMN  
 WIFRSVYIERPYLAMFGQVPSDVGDTTYDFAKCTFTGNESEKPLCVLEDRNLPRFFEWITTFVCLYMLSENILL  
 VNLLVAMFGYTVGTQVRNNDQVNRQRYFLVQEXCSRLNIFFFFIYFAYFYMVVKKCPRCKCKEKNMESVCCF  
 HNEEDNETLAWEGVMKENYLVKINTKANDESEMPRRFRQLDTRKINDLKSGLKRIANKIK

**Transmembrane domains.**

amino acids 681-701, 718-738, 734-754, 757-777, 784-804, 819-839, 853-873,  
951-971, 995-1015

**N-glycosylation sites.**

amino acids 6-9, 75-78, 247-250, 308-311, 812-815, 925-928, 1041-1044,  
1063-1066

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 83-86

**Tyrosine kinase phosphorylation sites.**

amino acids 21-27, 219-226, 279-286

**N-myristoylation sites.**

amino acids 71-76, 141-146, 174-179, 209-214, 299-304, 577-582, 643-648,  
904-909

**Amidation site.**

amino acids 102-105

104/162

**FIGURE 97**

RRGRGEVLAVERGSGSGGGGTPSGWPFAAAGADKKKPSRCGSGREGVSEGRKSMTGLYELVWRVYLHAECLHR  
TATSWLAVRFGTWNWIRROCCRAASAAYLAFLGFTLKKPPAVGKRRRRHRHPPGGSCLAARHHRMRNFADGRSL  
EKLPHVMGLVITEVEQEPSPFGDIASLVVWCMVGLISYISVDHQGTFRKNNRKLMDIELKQQQELLGLDCSKYS  
PEFANSNDKDDQVLNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQRRPTOLDVDTLASLLSSRGCPDFDLVL  
KEGPVDSTLGLFEPWHIRLLEIVSLPSHLNISTYEDFFSALRQYAACEQRLGK

**Transmembrane domain.**

amino acids 166-186

**N-glycosylation sites.**

amino acids 198-201, 325-328

**Glycosaminoglycan attachment sites.**

amino acids 14-17, 16-19

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 34-37, 270-273

**N-myristoylation sites.**amino acids 13-18, 18-20, 17-22, 19-24, 20-25, 47-52, 123-134, 156-161,  
215-220



105/162

**FIGURE 98**

MTGLYELVNRVLNALLLHRTLTSLRVRVFGTNWNIWRCCPAASAAYLAPLGFTLRKPPFVGRNRNRHRRPRG  
GSCLAAAHHRMRWRADGRSEKLPVHNGLVITEVEQEFSFSOIASLVVHCNAVGISYLSVYDHQGI FKRNSKL  
MDEILKQQRLLGLDCSKYSPEFANSNEKKDDQVLNCHLAVKVLSTEDGKADIVRAAQDFCQLVAQKQKRPTDLD  
VDTLASLLSSNGCPLDPDLVLRFGFVDSIRGFLPMHIRLTEIVSLPSHLNISYEDFFSALPQXACEQRLEG

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 115-132

N-glycosylation sites.

amino acids 144-147, 271-274

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 216-219

N-myristoylation sites.

amino acids 75-80, 102-107, 161-166

106/162

**FIGURE 99**

MYQRLWYSKILRRRKQAQLLLVHLITFGLEVCLARGITYVPFLLEVGVRKKFNTMVLGIGPVLGLVCVFLGSA  
SDHWKRGVYGRRRPPIWALSGLILLSFLIPKAGWLAGLCPDPRFLALALLLGVSILLDFCGQVQCFTPLEALLS  
DLFRDPDHCQAYSVYAFMISLGGCLGYLLPATWDTALAPYLGSTQECLFGLLTLILTLTCAATLLVAEEAA  
LGPTFPAEGLSAPSLSPHCPCCRAKLAFRNLGALLPRLHQLCCRMPTLRRLFYAELCSMMALMTFTLFYTDV  
GEGNLQGVPRAEFGTEARRHYDEGVRMGSLGLFLQCAISLVFSLVMDRLVQRESTRAVYLASVAAFPVAGATC  
LSHSVAVVTASALTGETFSALQILEYTLASLYHREKQVFLPKYRGDTGGASSEDSIMTSFLPGPKPGAPFPNG  
HYGAGGSGLLPEFFALCGASACDVSRRVVVGEFTEAKVVPGRGICLDLAILDSAFLLSQVAFSLFMGSIVCLSQ  
SVTAYMVSRAIGCLVLIYFATQVVFDSULAKYSA

**Signal sequence.**

amino acids 1-35

**Transmembrane domains.**amino acids 15-35, 52-72, 87-107, 122-142, 160-189, 240-260, 277-297,  
321-341, 486-506, 521-541**N-myristoylation sites.**amino acids 27-32, 95-100, 171-176, 299-304, 303-308, 320-325, 419-424,  
447-452, 462-467**Amidation site.**

amino acids 82-85

**Cell attachment sequence.**

amino acids 415-417

107/162

**FIGURE 100**

MAAIRRLGAAILLLPLLAAYETIMDSSTATATAGLNMVHPPSGWEEVSGYDENRNTLATYQVCNVFESSQNNWLR  
 TKPIRRRGAHRTHVEMKFSVRCSSIPSVPGSCKRTNLYYYEADFSATKTFPNNMENFWKVDITIADESF  
 QVDLGGKRVKINTEYRSFEGVSRSGFYLAQDYGGCMBLIAVRVYKCPRTTONGCAIFQETLSGAESTSLVAA  
 RSGCIANAREHVDPILKLYCNGDGEWLTFIGRCMKKAGFEAVENGTVRCGCPSTFRANQSGDEACTHCPINSRTT  
 SEGATHVCVRUGYRADELDLDMPTTTPSAFQAVITSSVNETSMLBMTTPPDSSGGREDLVNTTICKSCGSGRG  
 ACTRCGDNVQYAPFQGLTEFRIYISDLLAHTQYTFEIQAVNGVTDQSFPSPQFASVNTTNGARFSAVSIMHQ  
 VSRFVDSITLSWSQPDQNGVILQYELQYXERKELSEYNATAIKSPNTVTVQGLKAGAIYVEQVARTVAGYGR  
 YSGKMYFQTMTEAEYQTSIQEKLPLITGSSAAGLVFLIAVVVIAIVCNRRRGRFERADSETDKLQHTYSGHMTF  
 GMKXIYIDPFTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLPLPGKRETFVAIKTLKSGYTEKQRR  
 DFLSEASINGQFDHFNVIHLEGVYTKSTPVMIIITFMENGSLDSFLRQNDGQFTYIQLVGMRLGRIARGMKYLAD  
 MMYVVRDLAARNILVNSHLVCKVSDGSLRFLDDTSDPTYSALGGKPIKWTAPETAIQYRKFTSASDVWSYG  
 IVMHEVMSYGERPYNDMTNQDVINATIEQDYRLPFPMDPCPSALHQLMLDCWQKDRMHRKFTGGQIVNTLDMIRNP  
 NSLKAMAPLSSGINLPLLEDTIPDYTSFNTVDENLEAIKMGQYKESFANAGFTSFDDVVSQMMEDILAVGLTIA  
 GRQKKILNSIQVMRAQMNQIQSVEV

**Signal sequence.**

amino acids 1-18

**Transmembrane domain.**

amino acids 542-562

**N-glycosylation sites.**

amino acids 265-268, 336-339, 428-431, 482-485, 705-708

**Glycosaminoglycan attachment site.**

amino acids 367-370

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 802-805

**Tyrosine kinase phosphorylation sites.**

amino acids 374-381, 595-603, 736-743

**N-myristoylation sites.**amino acids 182-187, 213-218, 224-229, 271-276, 275-280, 299-304, 366-371,  
 497-502, 546-551, 706-711, 726-731, 730-735, 875-880, 958-963**Amidation site - amino acids 644-647****Tyrosine protein kinases specific active-site signature - amino acids 743-755**

Receptor tyrosine kinase class V signature 1 - amino acids 182-198

Receptor tyrosine kinase class V signature 2 - amino acids 241-261

Ephrin receptor ligand binding domain - amino acids 20-197

Protein kinase domain - amino acids 622-881

Fibronectin type III domain - amino acids 325-421, 436-520

SAM domain (Sterile alpha motif) - amino acids 912-976

108/162

**FIGURE 101**

MALPRIGAAALLLLPLLAARVEETLMDSTTATAGLGMVHPSPQWEEVSGYDENMMNTINTIQVCNVFESSQANWLR  
 TETIRRRGAHRINHEMKFSVGRDSSIPSVFSGCKETIFELYYEADPDSATKTFPNNMERFWYKVDITLAADESPS  
 QYDLGGCRVMKINTVTVRSFGFVSGSGFYLAQDYGGCNSLIARVVFYRKCPRTIQNGAIPQETLSGAESTSLVAA  
 RGSCLIANAEVVDVPIHLKYNCGDGGZWLVPFGKCMCKAGFAVENGTVCBGCFSGTFKANQGDEACTHCPINSKT  
 SEGAGNCVCNNGYXRADLPIDMPCTTIPSAPOAVIGSSVNETSLHLEWTFPRDGGGREGOLVYNIICKSCGSGRG  
 ACTRCGDNVCQYARPOLGLTEPRIYISDLIARTQVTEICAVNGVTDQSPFSPQFASVNHITTTGAAPSAVSIMHQ  
 VSKTVDSTLSSQSPDQFNGVILDELYQYERKELSEYNATAIKSPTHVTYVQGLKAGAYVVFQNKARTVAGYGR  
 YSGTWISQTMTEAEYQTSIOEKLFIIGSSAAGLVFLAVVVVATVCNRRGFRADSEYTKDLQHTSGHMTFG  
 MMYIYIDPFYIEZOPNEAVKREFAKEIDISCVKISQVIGAGEFGEVCSGHLKLPKGTEIFVAIKTEKSGVTEKQKQ  
 FLSEASIMGQFDHFWIHLGCVVTKSTPFVMIITEFNENGSLSDFLRNDGQFTVIQLVGOMERGTAAGMKYLADM  
 NYVVRADLAARNTILYNSHLGVCKYSDFLGSRLEDDTSDFTYTSALGGKIFIKWTAPRAIQYRKFTSASDVWBYGI  
 VMWEVMSYGERPYWDMTHNQVINALEQDYRLPPPMDCFSALHQLMLDCWQKDRNRHPKFGQIVNTLDKMLRNPN  
 SLKQMAPLSSGINLPLLDRTIFDYSFNTYDERLEAKRGQYKESFANAGFTSFLVVSQMMRELILRVGVTLAG  
 RQKKILNSIQVMRAQMNQIGSEV

**Signal sequence.**

amino acids 1-18

**Transmembrane domain.**

amino acids 543-563

**N-glycosylation sites.**

amino acids 265-268, 336-339, 428-431, 482-485, 704-707

**Glycosaminoglycan attachment site.**

amino acids 367-370

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 801-804

**Tyrosine kinase phosphorylation sites.**

amino acids 374-381, 594-602, 735-742

**N-myristoylation sites.**amino acids 182-187, 213-218, 224-229, 271-276, 275-280, 299-304, 366-371,  
497-502, 546-551, 705-710, 725-730, 729-734, 874-879, 957-962**Amidation site.**

amino acids 643-646

**Tyrosine protein kinases specific active-site signature.**

amino acids 742-754

**Receptor tyrosine kinase class V signature 1.**

amino acids 182-198

**Receptor tyrosine kinase class V signature 2.**

amino acids 241-264

**Ephrin receptor ligand binding domain.**

amino acids 20-197

**Protein kinase domain.**

amino acids 621-880

**Fibronectin type III domains.**

amino acids 325-421, 436-520

**SAM domain (Sterile alpha motif).**

amino acids 911-975

**Src homology 2 (SH2) domains.**

amino acids 733-769, 787-797, 806-819

109/162

**FIGURE 102**

MMFSTSSSSFRYDREFLRLTLPGLIVAEIVLGLLVWTLIAGTEYERVPAPGWVMFVAVFYWVLTVFLLIYITM  
TYTRIPQVPFWITVGLCFNGSAFVLYLSAAVVDASSVSPERUSHNFNSWAASSFFAFVLNICYAGNTYFSLAWR  
SRNTQ

**Signal sequence.**

amino acids 1-41

**Transmembrane domains.**

amino acids 53-73, 86-106, 122-142

**N-glycosylation sites.**

amino acids 2-5, 92-95

**N-myristoylation site.**

amino acids 88-93

**Leucine zipper pattern.**

amino acids 17-38

110/162

**FIGURE 103**

MNFTSSSSSFAYDREFLETLPGFLIVAEIVLQLLVWTLIAGTEYFRVPAFGWVMFVAVFYWVLTVFLLIIXTM  
TXFRLPQVPWMTVGLCPNGSAFVLYLSAAVVDASSVSFERDSHWFNENSWAASSTFAFLVTICYAGNTYPSFIAR  
SKTIQ

**Transmembrane domains.**

amino acids 19-39, 53-73, 86-106, 122-142

**N-glycosylation sites.**

amino acids 2-5, 92-95

**N-myristoylation site.**

amino acids 88-93

**Leucine zipper pattern.**

amino acids 17-38

111/162

**FIGURE 104**

MPTTVDDVLEHGGEFRHFQKQMFELLALLSATFAPLIYVGIVFLGFTPDHRCRSPGVAEISLRGWSFAEELNYT  
 VPGVGPAGEASPRQCRRYEVDNNQSTFYDCTDPLASLDTNASRLPLGFCRDGWNVYETPGSSIVTETNLVCANSNM  
 LDELQSSVNVGFFIGSMISIGYIADRFGKICLLATTVLINAAAGVLMWISPTTWMILFRLIOGLVSKAGWLGX  
 ILITEFVGRRYRRTVGITFYQVATTVGLLVLAGVAYALEHWRWLQFTVALENPFFELLYWCIPESFRLISQNN  
 AEAAMDITPHIAKRNKSLPASLQRLREETGKKLNFSEFLVLVRTTQIRKHTMIIMYNWFTSSVLYQGLIMHMG  
 LAGTNIYLDFFYSALVEFPAPFMILLTIDRIGRRYFWAASNMVAGAACLASVFTPGDLQWLKIIISCLGRMGIT  
 MAYEIVCLVNAELIYPTFIHNLGVHICSSMCDIGSITTFPLVYRLTNIWLELPLMVFGVLGLVAGGLVLLVETK  
 GKALPETIEAENMQRPKRKNEKMIYLVQVKLDIPLN

**Transmembrane domains.**

amino acids 20-40, 174-194, 205-225, 238-258, 269-289, 351-371, 376-396,  
 412-432, 492-512

**N-glycosylation sites.**

amino acids 72-75, 97-100, 113-116

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 345-348

**Tyrosine kinase phosphorylation site.**

amino acids 536-553

**N-myristoylation sites.**

amino acids 191-196, 254-259, 442-447, 466-471, 504-509

**Amidation site.**

amino acids 174-177, 229-232, 327-330, 401-404

**Sugar (and other) transporter.**

amino acids 23-529

112/162

**FIGURE 105**

MPTTVDDVLEHGGEFFHQKQMFLLALLSATFFAITYVGIVELGFTPDHRCRSPQVAELSLACGWSFAEELMYT  
 VPGPGPAGEASPRQCRKYEVDRNQSTFDCVDEPLASLUTNKRSLPLGRCRDGWWVYETPGSSIVTEFNLVCANSWM  
 LQLEQSSVNVGFTFGSSISIGYIADRSGRKLCLLTTLVINAAGVIMAISFTYTNMLIFRLTQSLVSKAGNLIGY  
 ILITEFVGRYRRTVGIFVQVATVGLLVLAGVAYALPHNRNLQFTVSLPNTFFLLXYWCIPESPPMLISQMKN  
 ARAMRIIKHIAKINGKSLPASLQRLBLESETGKKLNPSFLDLVPTPQIRKHTMILMYNWETSSVLYGGLINAMG  
 LAGUNINLDFFYSALVEFFAAPMIILTIURIGRRYPWAASHNVAGAACLASVFIPGDLQNLRIIISCLGRMGIT  
 MAYEIVCLVNAELYPTFIRNLGVHICSSMCDIGGIITPFLVYRLNINWLELPINVFGVLGLVAGGLVILLPETK  
 GKALPETIEARENMQPPKKKERTMIYLQVQKLDIPLN

**Transmembrane domains.**

amino acids 20-40, 174-194, 205-225, 230-250, 269-289, 351-371, 376-396,  
 412-432, 492-512

**N-glycosylation sites.**

amino acids 72-75, 97-100, 113-116

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 345-348

**Tyrosine kinase phosphorylation site.**

amino acids 536-544

**N-myristoylation sites.**

amino acids 191-196, 254-259, 442-447, 466-471, 504-509

**Amidation sites.**

amino acids 174-177, 229-232, 327-330, 401-404

**Sugar (and other) transporter.**

amino acids 23-529



113/162

**FIGURE 106**

MAPWPELGDAQPNFQKYLEGANGQQPTAPDKSKETNKTDNTEAPVTKIELLP9VSTATLIDEPTTEVDDPWNLEF  
 LQDSGIKTYSERDETKKILCFPQGLGRLLLLGLFLYFFVCSLDILSSAFQLVCGKMGQFFSNSSIMGNPILGLV  
 IGVLVTVLVQSSSTSTSIIVSMVSSSLITVKAAPFIMGANIGTSLTNTIVALMQVGRSEPRRAFAGATVADF  
 PNWLSVLNLLPVEVATHYLEIITQLIVESTHFMINGEDAPDLLKVTTKFTKLIVQLDKKVISQIAMNOEKAKNK  
 SLVKINCKTFTENKTQINVTVPSTAHCTSPSLCWTDPQIQNWTMKNVTYKENTAKCGHIFVNFHLPDLAVGTLLI  
 LSLVLVCGCLIMIVKILGSVLKQVATVIKRTINTDFFPPFANLITGYLAILVAGMTFTVQSSSVFTSALTPLI  
 GIGVITIERAYPLTQSNIGTTTALLAALASPGNALSSSLQIALCHFFFNISGILLWYPIPETRLPIRMAGGL  
 GNISAKYRWFVAVFLIIFPFLIPITVFGLSLGRVVLVGVGVVFTIILVLCRLQLSRCPVLPKKLQWNNF  
 LPLNMRSLKFPNDVAVSKFTGCFQMRCYCCVCCRACCLCGCPKCCRCCKCEDLEEAQEGGVFVKAPETFD  
 NITTSREAQGEVPA5DSKTECTAL

**Transmembrane domains.**

amino acids 96-116, 136-156, 178-196, 219-239, 356-376, 372-392, 406-426,  
 445-465, 488-508, 523-543, 549-569, 565-585, 592-612

**N-glycosylation sites.**

amino acids 36-39, 136-139, 295-298, 308-311, 313-316, 321-324, 335-338,  
 340-343, 495-498, 520-532, 667-670

**N-myristoylation sites.**

amino acids 23-28, 79-84, 126-131, 131-136, 146-151, 150-159, 187-192,  
 191-196, 393-398, 423-428, 460-465, 464-469, 519-524, 546-551, 634-639

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 635-646

**Insulin family signature.**

amino acids 621-635

**Heat-stable enterotoxins.**

amino acids 617-633, 625-641, 613-629

**Na<sup>+</sup>/Pi-cotransporter.**

amino acids 118-549

114/162

**FIGURE 107**

MAPWPELGDAQPNPDKYLEGAAGQQOFTAPDKSKETNKTONTTEAPYTKIELLESYSTATLIDEPTENDOPWNLPT  
 LQDSGILWSEEDTKGKLLCFQGGIGRLILLLGLYFFVCSLDLSSAFQLVGGKMAQQFFSNSSIMSNPLLGIV  
 IGVNTVVLVQSSSTSTSIIVSMVSSSLTVRAAIPINGANIGTSITNTIVALMQVGDRSEFFRAFAFAGATVHDF  
 FNLGLSVLILFLPVEVATHYLEIITQLIVESFHNKNGEDAROLLKVITKPETKLIVQLDKKVISQIAMMDEKAKNK  
 SLVKINCHTFTNKTQINVTVPSTANCTSPSLCWTDSIQNWTMKQVITYKENIAKCCQHFVNFHLPDLAVGTILLI  
 LSLVLCCCLIMIVKILGSLVLEQVATVIKKTINTDFPPFANLIGYLAILVQAGMTFIVQSSSVFTSALTPLI  
 QIGVITIERAYPLATGSGNIGTTTTAILAALASPGNALASSLQIALCNFFHISGILLWYEIPFTLPIRMAGKL  
 GMSAKYKWFVAVFYLTITFEFLILFLTVFGLSLAGWRVLVGVGVFVVFIIILVLCRLQLQSRCPVLEPKKLQNNWF  
 LPLWHRSLKPDWDAVSVKFTGCFQMRCCCCRVCCRACCLCGCPKCCRCCKCCDLERAQEGQDVPVKAPETFD  
 NITISREAQGEVPASDSKTECTAL

**Transmembrane domains.**

amino acids 96-116, 136-156, 176-198, 219-239, 356-376, 372-392, 406-426,  
 445-465, 488-508, 523-543, 547-567, 563-583, 592-612

**N-glycosylation sites.**

amino acids 36-39, 136-139, 295-298, 308-311, 313-316, 321-324, 335-338,  
 340-343, 495-498, 520-523, 667-670

**N-myristoylation sites.**

amino acids 23-28, 79-84, 126-131, 131-136, 146-151, 150-155, 197-192,  
 191-196, 393-398, 423-428, 460-465, 464-469, 519-524, 546-551, 634-639

**4Fe-4S ferredoxins, iron-sulfur binding region signature.**

amino acids 635-645

**Insulin family signature.**

amino acids 621-635

**Na<sup>+</sup>/Pi-cotransporter.**

amino acids 118-549

115/162

**FIGURE 108**

MWSGWRIWFLVAVCTADFFRDEAEKIMKDSFVIDGHNULFWQLLDMFNRLQDERANLTTLAGTHTNIPKLEAG  
FVGGQFWSVYTPCDTQNKDAVERFTLEQMDVVHFMCRMYPETFLYVTSAGIQAFRECKVASLIGVEGGHSIDS  
SLGVLRALYQLGMRKYLTLTSCNTPWADNWLVDVTGDSSEPOSGQLSPFGQRVVKELNRLGVLIIDLANVSVATMKA  
TLQLSRAPVLFPSHSSAYSVCGRSRNVFDDVLRVVKQTDLSVMVNFYNNHYISCTNKANLSQVADHLDRIKEVAGA  
RAYGFGGDFDGVPRVFEGLEDVSKYFDLIAELLRRNWTAEVKGALADNLLRVFGAVEQASNLTPAPEEETPL  
DQLGGGSCRTHYGYSGAGSSLRHWGLLASLAPLIVICLSLL

**Signal sequence.**

amino acids 1-16

**Transmembrane domain.**

amino acids 392-410

**N-glycosylation sites.**

amino acids 57-60, 279-282, 332-335, 358-361

**Tyrosine kinase phosphorylation site.**

amino acids 110-118

**N-myristoylation sites.**

amino acids 63-68, 76-83, 124-129, 139-144, 151-156, 375-380, 395-400

**Leucine zipper pattern.**

amino acids 390-411

**Renal dipeptidase active site.**

amino acids 140-162

**Renal dipeptidase.**

amino acids 1-411

116/162

**FIGURE 109**

MSQSNFFHATFVLIGLIGLEKAEFWVGFPILLSMYVVMFGNCIVVFYVRTEPSLHAEPLYFLCMLAIDLALST  
STMFKILALEWFDRELSFEACLTQMFFIHLSATESILLAMAFDRYVAICHFLRHAADVNNVTVAQIGIVAV  
VRGSLFFFPPLPLLIKRLAFCHSNVLSHSYCVHQDVVKLAYADTLPHVVYGLTALLVMGVDMVFISLSYFLILP  
TVLQLPSKSERAKAFGTCTVSHIGVLAFFYVPLIGLSVVERFGNSLAPIVRVVMGDIYLLLPVIMPILYGAKTK  
QIRTRVLAMFKTISCDKDLQAVGSK

**Transmembrane domains.**

amino acids 26-46, 57-77, 95-116, 144-164, 197-217, 238-258, 272-292

**N-glycosylation sites.**

amino acids 5-8, 136-139

**N-myristoylation site.**

amino acids 18-23, 238-243, 245-250

**7 transmembrane receptor (rhodopsin family).**

amino acids 40-131, 212-291

117/162

**FIGURE 110A**

MRILKKFLACIQQLLCVCRLDWANGY YRQQRKLVEEIGWSYTGALNQNKGWKYPCTCMSPKQSPFINIDEDLTQVN  
 VNIKKLKFQGRDKTSLIENTPIHRTGKTVEINLTHDYRVSGGVSEMVFKASKITPHWGRCKNMS3DGSSESLGGQK  
 FPLEMQIYCFDADRFSSEFAEVKGGKLRALSTLFEVGTSEENLDFKALLOGVESVSRFGQALDPPIILLNLLP  
 NSTDKYIYNGGSLTSPPTDTVQWTVFRITVSI9ESQLAVFCEVLTMOQBGVYMLMDYLQNNFRQZYKFSRQV  
 SYDYGKGEIEHRAVCSSEFFRVQADPENTISLLVTWERPRVVYDENTIEKFAVLXQQLDGEDQTKHEFLTDGYQD  
 LGAILNLLPRMYVLIQIVACINGLYGYKSDGLIVMPTDMPFLDLPELIGETEEIIEKEEEGKUIEGGAIVN  
 EGRDSATNRIRKKEPQIQTTHYNRIGTKYNEAKTNRSPTKSGSEFSGRGDVFNTHINSTSQPVTKLATEKUISL  
 TSQTYTPELPPHTVGGTSASLNDGSKTVLRSPHNNLSGTAESLNTVSI7EYEESSLLTSFKLDTGASDSGSGSFA  
 TSIIPFISENI9QCYIFQSENPTITTYDVLPRASARNASDSTSSGSESLKDPDSMEGNVWTFSSDTITAQPDV  
 QSGRFSFQYQNTMYETIRVDSEKPTKSFBAQVMSQGSVTDLEMPGYSTPAYFTEVTPHAFTPPSRQDOLVST  
 VNVVYSGITQYQVNGEITELQPSYSSEVFELVTPHLLQNLINATTPAASSSDSALEATPVFSSVDVSFESILSY  
 DGAFLFLPSSASFGSELEKHLKSVBQLLPQVTSATECKVPLASLPAVGGDILLLEPSLAQYSDVLSTTHAASE  
 TLEFSEBSGVLYKTLMTQVVEFPSSDMMHAPSSGPEPSYALSDNEGGQHTFYVYS8AIPVHDSVGVTVQGS  
 FSGPSHJPIPKSLLIPTASLLQPTALSGDSESVTSMNMYDVKINKASIQSTVSIGSTKCMFPFGSLANTTKV  
 DNKALSKSEIYGNETELQLFSNEMVYPSSESTVMNMYDVKINKASIQSTVSIGSTKCMFPFGSLANTTKV  
 FQHEISQVPENNFSQVPTHTVSQASGVTSLKPVLEANSSEFASDPSASSEMILHSTVSVPFVDSVTSMHASLQ  
 SFQASDVLTKLTVLPATVPSDFILVETFKVDKISSMLALLIENASSEMILHSTVSVPFVDSVTSMHASLQ  
 GQLSLVAGEKKEVPLKESSEHGVVPSLYSNDLEFQTANLEINQAHPPKGRHVEATFVLSIDEPILNTINKLIH  
 SDELLIYSTKSSVTGKVEAGTPTVASTDFVSTDSVFIQNGHVALTAVSPHSDGSVSTYKLLFPSKATSELS8A  
 SKDAGLVGGGSDGDTDDGDDDDURDS DGLSIHKCHSC8AYRESQKVMNDSGTTHENSIMQNNITYS3LSENS  
 EENRVTVS5SDSGSTGMDSRSPGKPSANGLSQKHNDGKEENIQTG8ALLFLSPESHAWAVLISUEKSGSGQGT  
 SDLSNENETSDPSFADTRKDKSGDGLIAGDSEITPGFPQSTSSSVTSENSEVFVHVS8A8ASNS8SES8IGLAE  
 GLESEKAVIPLVIV8ALLFFCIVVILGILYWRKCPQTA8FLRDSST8P8V8STPTPTPTPT88D8V8AIFLKH  
 FPKHVALDL8AS8GT8E8PTLKEFTYQVQ8CTVPLG8ITAD88NH8DKH8HRYINIV8YD8SRVLA8LAEK8G  
 KLT8VIN8MY8GYN8K8AYL8AQ8PLK8TAE8D8W8M8I8E8N8VE8IV8M8L8N8I8E8K8R8K8Q8Y8N8P8D88E8Y8N  
 FLV8TK8SV8V8LAY8TV8RN8TL8N8TK8K8G8SK8K8P8GR8V8TV8QY8Y8TK8Q8P8M8G8V8T8SL8P8VL8TV8V8K8AY8K8RA  
 V8P8V8V8V8C8AG8V8GT8TY8IV8D8ML8Q8I8Q88G8TV8N8IF8G8FLK8I8S8Q8N8Y8LV8Q8E8Q8Y8PI8D8TL8E8A8L8K8E8T8  
 V8D8A8I8AY8V8N8ALL8PG8AG8TK8LE8Q8F8QL8S8Q8N8I8Q8SD8Y8A8LK8Q8C8N8R8K8N8T8S8I8P8V8S8R8V8G8S8S8L8G8E  
 GT8D8Y8IN8SY8M8GY8Q8N8E8I8T8Q8P8L8AT8IK8D8W8R8M8I8W8D8N8AQ8LV8M8IP8G8Q8N8A8E8D8F8Y8W8N8K8D8E8F8I8N8C8E8F  
 K8V8T8M8A8B8E8K8CL8S8E8K8E8I8Y8Q8D8F8LE8AT8Q8D8Y8V8LE8V8R8F8Q8P8K8W8P8D8P8I8K8T8F8EL8SV8I8E8A8A8N8D8G8M8I8V  
 H8E8H8G8V8TAG8T8F8AL8T8TL8H8Q8LE8K8NS8D8V8Y8Q8V8AK8M8I8M8R8F8G8T8AD8EQ8Q8FLY8K8I8SL8V8TR8Q8E8N8P8T8L8I8  
 D8N8C8A8LP8G8N8I8A8S8E8SV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain.**

amino acids 1638-1658

**N-glycosylation sites.**

amino acids 105-108, 134-137, 223-226, 232-235, 324-327, 381-384, 497-500,  
 501-504, 552-555, 602-605, 629-632, 677-680, 1017-1020, 1050-1053, 1082-1085,  
 1122-1125, 1456-1459, 1561-1564, 1617-1620, 1868-1871, 2051-2054, 2078-2081

**Glycosaminoglycan attachment sites.**

amino acids 490-493, 991-994, 1548-1551, 1550-1553, 2076-2073

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 1877-1880

**Tyrosine kinase phosphorylation site.**

amino acids 148-156

118/162

**FIGURE 110B****N-myristoylation sites.**

amino acids 139-144, 186-191, 372-377, 471-476, 486-491, 533-538, 555-560, 582-587, 588-593, 638-643, 893-898, 960-965, 1087-1102, 1259-1264, 1385-1390, 1411-1416, 1415-1420, 1549-1554, 1551-1556, 1553-1558, 1579-1584, 1625-1630, 1879-1884, 1935-1940, 2123-2128, 2225-2230, 2226-2231, 2230-2235

**Amidation sites.**

amino acids 49-52, 1831-1834

**Tyrosine specific protein phosphatases active site.**

amino acids 1930-1942

**Protein-tyrosine phosphatase.**

amino acids 1749-1990, 2047-2280

**Eukaryotic-type carbonic anhydrase.**

amino acids 38-360

**Fibronectin type III domain.**

amino acids 312-401

**MAM domain proteins.**

amino acids 1757-1785, 1060-1068, 1813-1853, 2047-2079

119/162

**FIGURE 111**

MCARMAGRTRAAPPGPYGFNLCLLVALALDQVVRVDCGQAFIDPVYLVHTAARPAQFTLTWAKLDRFKGSRHHTT  
 LITCHRAGLTEPDSSSPLELSEFLWVDFVVENSTGGGYAVTRPVTWQLEYPGQAPAEKQDMVWEILVSEKUR  
 ALIPLAKAEELVNTAFPLTGVPQHVPVRLVTVDGGGALVEVTEHVGCESANTQVLQVSEACDAVFFVAGKESRGAR  
 GVRVDFWKKRLRASRLTVMAPLLPLRIELIDTTLEQVRGKVRVPGPAEGPAPAAEASDEAERRRARGCHLQYQR  
 AGVEFLAPPAAARPDGGRRITHLGPDWLLDVSHLVAFHARVLDQKVASLEGGGVRVVGREPGVTSIEKVSFLSD  
 SILGEQALAVTDDVSVLELRVQPVMTSLTISRGTANFGEVTRATCWAQSALPAPRQEVALSQWLSFSDSTVAP  
 AELVDRDLGLSVSAETPCATLPAEDQGAQLGVVSVSAGAEGLPLAVALHPPEPCRRGSHVPLASGTAWLGLF  
 PASTRAPALPSSPANSFPATEATMTGGKQVAGSVGNTGVRGKTERAEENARKEETEAREEEEEEMVPAFQ  
 RVTELELGMVALLGVFCVAIFITLVNGVVVFVLYQRKEPPYDSATDPTSPQPHNVWLTDQKELSQLDRQSPG  
 PFKGEGSCPCESGGGGEAPTLAPGPPGGITSSSETLARKSAGGRKRVEFVTFVPAPPAQSPREPVGAPAVQSI  
 LVAGEERDIRWVCEDMGLKDPRELNYMERINGSS

**N-glycosylation site.**

amino acids 106-109

**Glycosaminoglycan attachment sites.**

amino acids 480-483, 678-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 314-317

**Tyrosine kinase phosphorylation site.**

amino acids 758-766

**N-myristoylation sites.**amino acids 109-114, 111-116, 193-198, 397-402, 454-459, 472-477, 476-481,  
 516-521, 550-555, 553-559, 672-677, 693-698, 694-694**Amidation sites.**

amino acids 312-315, 543-546, 708-711

120/162

**FIGURE 112**

MATKTELSPTARESKNAQDMQVDETLIPRKGPSLCSARYGIALVLRFCNFTTIAQNVIHNIHVMVHNTSPQS  
QLNDSSEVLEFVDSFGGLSKAPKSLPAKSSILGGQFAIWEKRGPPQERSRILCSIALSGMLLGCFTAILTGQFLSE  
TLGNFVFVYIFGGVGCVCCLIMEFVVIYDDPFSPWISTSENEYIYSSLKQGVSSSKQLPIKAMLASLFWISIC  
LGCPSSHQWLVSTMVVIYPTIYISSVYHVNIRONGLSALEFTIVANVIGMVGGYLAADPILTKKFLITVVKIATIL  
GSLPSSALIVSLFYINSGYITATALLTSLCGLSTLCQSGIYINVLQIAPRYSSFLMGASRGFSSTAFVIVPTVS  
GFLLSQDFEFGRNRNVFLLFAVNLLGLLEYLIFGEADVQENAKERKLTRL

**Transmembrane domains.**

amino acids 124-144, 154-174, 255-275, 287-307, 319-339, 350-370, 385-405

**N-glycosylation sites.**

amino acids 49-52, 60-63, 68-71, 77-80

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-418

**N-myristoylation sites.**

amino acids 106-111, 131-136, 135-140, 143-148, 160-165, 163-169, 255-260,  
269-274, 272-277, 297-302, 325-340, 353-358



121/162

**FIGURE 113**

MQVDETLPKRVPSLCSARYGIALVLHFCNFTTIAGNVIMNITMVMVNSTSPQSQLNDSSEVLVDSFGGLSK  
APKSLPTKSSITLGGGFATNEKNGPPQERSRLCSIALSGMLLGCFTRAILGGFTSETLGNPFVFIYFGVGVCVCC  
LLWFVVIYDDPVGYPIWISTSEKEYTISSLKQGVRSRQGLPIKAMLRSLPIWSICLQCFSHQWLNSTMVVIPT  
YISSVYHNRUNGSLGSLPFTIVAWVIGMVGGYLADFLLEKKERLITVRKIATILGSLPSSALIVSLPTLNSGY  
ITATALLTSLCGSLTLCQSGTIYINVLDIAPRYSSFLWQASRGFSSIAFVIVPTVSGFLLSQDEPFQWRNVFELL  
FAVNLGLLFLYLIHQEADVQEWAKERKLTRL

**Transmembrane domains.**

amino acids 22-42, 105-125, 137-157, 236-256, 268-288, 300-320, 331-351,  
366-386

**N-glycosylation sites.**

amino acids 30-33, 41-44, 49-52, 58-61

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 396-399

**N-myristoylation sites.**

amino acids 87-92, 112-117, 116-121, 124-129, 141-146, 144-149, 236-241,  
250-255, 253-258, 278-283, 316-321, 334-339

122/162

**FIGURE 114**

MAGAGPKRRALAAPAAEEKEEAKERMLAAKSADGSAAPAGEGCVTLQRNITLINGVAIIIVGTIIGSGIFVTPFG  
 VLKERAGSPGLALVWNAACGVFSIVGALCYAEELGTTISKGGDYAXMLEVYGSLEAPLELWLELLIPPSQYIV  
 ALVFPATYLLKELEPFTCFVPEBAKLVACLCLVLLLTAVNCYSVKAAFRVQDAFAAKLLALALIIILGFGVIGKG  
 DVGNLDEKFSFEQTKLDVGNIVLALISGLFAYGGWNYLNFVTEEMINPYRNLPLAIIISLPIVTLVYVLTNLAY  
 FTTLSTEQHLSSERVAVDPFONYHLGVMSWLLFPVVGLCFCGSGVNGSLFTSSRLFFVGBREGHLPSILSMIAPQL  
 LTPVPBLVFTCVMTLLYAFSKDIFSVINPFSTFNNLCVALAIIGMIWLRHRKPELERPIKVMILALPVFFILACL  
 FLIAYSVWKTPEVCGIGITIIISGLPVYPTGVWWRNKPKWLLQGIFSTTVLCQKLMQVVPQET

**Transmembrane domains.**

amino acids 48-68, 83-103, 120-140, 137-157, 165-168, 200-220, 236-256,  
 274-294, 316-336, 364-384, 394-414, 430-450

**N-glycosylation sites.**

amino acids 49-52, 340-343

**Tyrosine kinase phosphorylation site.**

amino acids 112-119

**N-myristoylation sites.**

amino acids 34-39, 61-66, 107-112, 114-119, 125-130, 337-342, 341-346,  
 353-358, 459-464, 488-493

**Amino acid permease.**

amino acids 46-481

123/162

**FIGURE 115**

NAGAGPKRRALAAPAAEKKEEAREKMLAKSADGSAPAGEGGVTLQRNITLLNGVAITVGTITIGSGIFVEPTG  
 VLKEAGSPGLALVYVRAAGVFEIVGNLCYAEAGTTISKGGDYAYMLEVYGSLEAEFLKLWIELLIITPSSQYIV  
 ALVFRTYILLKPLFFTCVPPEEAARKLVACLCULLLTFVNCYSVKAATRVQDAFAAAKLLALALLILLGFVQIGKG  
 UVSNLDPNFSFEGTKLDVGNIVLALYSGLFAYGGWNYLNFVTEMINPYRNLPALIIISLPVTLVYVLTNLAY  
 FTTLSTEQMLSSAEAVAVDFGNHYHLGVMSWYLPVFVGLSCFGSVNGSLFTSSRLFFVGSREGNLP SILSMINPQL  
 LTPVPSLVFTCVMTLLYAFSKDIFGVINFFSFENWLCVALAIIGMINLRGRKPELERPIKVNLAFLVPPILACL  
 FLIAVSEWTKTPVECGIGETIILSGLPVYFSGVWKKPKWLLQGIFSTTVLCQKMLQVVFQET

**Transmembrane domains.**

amino acids 48-69, 83-103, 120-140, 137-157, 165-185, 199-219, 235-256,  
 274-294, 316-336, 364-384, 394-414, 430-450

**N-glycosylation sites.**

amino acids 49-52, 230-233, 340-343

**Tyrosine kinase phosphorylation site.**

amino acids 112-119

**N-myristoylation sites.**

amino acids 34-39, 61-66, 107-112, 114-119, 125-130, 337-342, 341-346,  
 353-358, 459-464, 488-493

**Amino acid permeases.**

amino acids 46-481

124/162

**FIGURE 116**

MALEPTARPLLGSQCTPALGSLLELLFSLGWVQPSRTLAGETGQEAAPLDGVLARPPNIGSLSPRQLLGFPFAEV  
SGLSTERVREIAVALAQKNVKLSTBQLRCLAKRLSEPPEDIDALPLDLLFLNPDAPFGGPQACTRFFTSRYTKAN  
VDLELPAGAPERQRLLFAALACMGVGRGSLLEADVRALGGGLACDELPGRFPVAESADEVLLPKLVSCPGPLDQDQQA  
ARALQGGGCPYPGPPSTWSTVMDALNGLLFVLGQPIIKSIQGSIVAANRQSSRDPSWQPFERTILRPFRRE  
VEKTACPSGKKAREIDESLIPTKWELEACVDAALLATQMDRVNAIPETTYEQLDVLKHKLEDELYPQGYPSVIQ  
HLGLVFLKMSPEDIPKWNVTSLLETLKALLEVNRGHEMSTQVATLIDRFVRGRGQLKDTLDTLTATYPGYLCSL  
SPHELSVPPSSWAVRPQDLTDCPRQLDVLYPKARLAFQNMNGSEYFVKLQSFLLGQARTEDLKALSQQNVSM  
DLATFMKLRTPDAVLPLEVAEVQKLLGPHVEGLKAEERHSPVFRWILRQRQGLDDELGLGLQGGIIPNGYLVLDLS  
VQBALSGTFCLLGPGPVITVYALLASTLA

**Signal sequence.**

amino acids 1-33

**Transmembrane domain.**

amino acids 603-621

**N-glycosylation sites.**

amino acids 57-60, 388-391, 488-491, 515-518

**Tyrosine kinase phosphorylation site.**

amino acids 353-360, 471-477

**N-myristoylation sites.**amino acids 171-176, 174-179, 186-191, 266-271, 501-506, 577-582, 580-585,  
581-586**Amidation site.**

amino acids 304-307

**Leucine zipper pattern.**

amino acids 101-122

125/162

**FIGURE 117**

MALPTARPLLGSCTPALGSILFLFLFBLGNVQPSRTLAGETGQEAAPLDGVLANPPNISSLSLSPQLLGGFPCAEV  
 SGLSTERTVRELAVALAQRKNVKLSTQIACLAHLRLSEPPEDLDALPLDLLFLNPLDAPSGPQACTAFFSRITKAN  
 VDILPRGAFFERQRLLEPAALACWGVRSLLSEADVRALGGACDLPGRFVRESAEVLLPKLVSCPGPLDQDQQA  
 ARMALQGGGPPYQPPSTWVSVMALRGLLFVLGQPTIRGIPQGIWAARWRQSSRDPSWRQPERTILEPFRFEE  
 VERTACPSGCKAREIDESLIIFYKKWLEACVDAALLATQMDRVNAIPTTYEQLLVLRHKLDELXPCGYPESTQ  
 HLGVLFELKMSFEDIKRNVTSLETLKALLEVNKGHEMSQVATLIDRFVKGRCQLDKDTLDTLTAFYPGYLCSL  
 SPEELSSVFPSSINAVRPPQDLDTCDPQQLUVLYPKARLAFQNNNGSEYFVKIQSFLGGAPTEDEKALSQONVSM  
 DLATFMKLRTDVILPLFVRAEVQKLLGPHVRGLKAERRRFPVRDWILRQRQDELOTGLGLGQGGIPNGYLVLDLS  
 VQKALSGTPCLLGGPGVLTIVLALLASTLA

**Signal sequence.**

amino acids 1-33

**Transmembrane domain.**

amino acids 603-623

**N-glycosylation sites.**

amino acids 57-60, 388-391, 488-491, 515-518

**Tyrosine kinase phosphorylation sites.**

amino acids 353-366, 471-477

**N-myristoylation sites.**
 amino acids 171-176, 178-179, 186-191, 266-271, 501-506, 577-582, 589-585,  
 591-586
**Amidation site.**

amino acids 304-307

**Leucine zipper pattern.**

amino acids 101-122

126/162

**FIGURE 118**

MATTVPCGCRNGYKSEYYRLCDKADAWGIVLETVATAGVVTSAZMLTEPILVCKVQDSNRBRMLETQFLFLLG  
VLGIPLGLETAFTIIGLDGSTGPTFRFTLPGILFESICFSCLLAHAVSLETKLVRGRKPLSLVLITGLAVGFSLVQDVI  
ALEYIVLTHNRTNWNVFSLSAPRNEDFVILLTYVLFIMALTFLMSPTFCGSETGWKRHGANYLEMLLSIA  
IYVAVITLLMLPDPDFRNDFTILSSALAAAGWVFLLAYVSPFVLLTRQRNPHDYFVEDAFCKPQLVKKSYGVE  
NRAYSQSEITQGFETGDTLYAPYSTHFQLNQPPQMEFSIPRAHAMFGPYKDYEVKKKES

**Transmembrane domains.**

amino acids 30-50, 66-86, 98-118, 121-141, 157-157, 174-194, 212-232, 244-264

**N-glycosylation site.**

amino acids 153-161

**N-myristoylation sites.**

amino acids 8-13, 38-43, 80-85, 88-93, 102-107, 136-141, 201-206

**Amidation site.**

amino acids 124-127

**7 transmembrane receptor.**

amino acids 27-273

127/162

**FIGURE 119**

MIPFLMFSLLLLLIVNPIANNNHYDKILARSRIKGRDQGFNVCAQQLLGTTKKKYPSTCKHWYKKSICGQKFT  
 VLYECCPGYMRMEGKKGCPAVLPIDHVGTLGIVGATTQRYSDASKLPEEIEGKGSFTTYFAPSNEANONLDSG  
 IRRGLESNWNVELNALSHMINKRMLTKDLKNGMIIFSMYNNLGLFINHYPNGVTVNVCARIIBGNQIATNGV  
 VHVIDRVLTQIGTSIQDFLEABDDLSGTPAAATTSOILEALGRDGHFTLPAPTNEAFKELPROVLERFWGDKVA  
 SEALMKYNTILNTLQCSFESIMGGAVFETLEGHTIEIGCDGDSITVNGIKAVNRKGLVTNNGVINHLIGVLIPOSA  
 KQVIELAGKQQTTFPDLVAQLGLASALFPDGEYTLAPVNNAPSDDTLSHWQRLKLILQNHILKVRVGLNELY  
 NGQILETIGGKQLRVFYRTAVCIENSCEKSGSQCRNGAIIHFRSTIIRPAEKSLEKELKQDKRFSTFLSLLEA  
 ADLKELLTQPSDWTLEFVPTNDAFKGMTSEKELLINDKNALQNLILYHLETPGVFICRGTFEGVTIHLMTTQGSK  
 IFLKEVNDTLVNHMKSKESDINTNGVIRVVDKLLYPADTPVQNDQLEILNKLTKYIQIRFVRGSTFREIFV  
 TVYTTKILTKVVEPKIKVIEGSLQPIIKTEGPTLTKVKIEGEPEFKLIKEGETITBEVINGEPIIKKTKIIDGV  
 FVEITEKETREERIITGPEIKYTRISTGGGETEETLKKLLQEEVTKVTKFLEGGDGHLEFDEBLKELLQGGVTPV  
 RKLQANKKVQGSRRRLREGRSQ

**Signal sequence.**

amino acids 1-21

**N-glycosylation site.**

amino acids 599-602

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 507-510, 731-734

**N-myristoylation sites.**

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,  
475-481, 570-575, 768-773

**Fasciclin domain.**

amino acids 94-232, 496-630

128/162

**FIGURE 120**

MIPFLPMFSLLLLLLVNFMANNHYDKILASRIKGRDQGFNVCAQQILGTAKKYFSTCKNNYKKSIOGQKTF  
 VLYECCPGYMMRMGEGKCPAVLPIDHVGTLGIVGATTQRYSDASKLREEIEGKGSTTYFAPSMEAWNDLSD  
 IRRGLESHVNVVELLNALASHMINKRMLTKDLKNGMIIFSMYNNLGLFINHYPNGVVTNVCARITGNGQIATNGV  
 VHVVDVLTQIGTISQDIEREDDLSSFRAAAITSDILEALGRDGEFTLFAPTNKAFKLPFGVLIERINGDKVA  
 SEALMKYHILMTLQCCSESIIMGAVFETLEGNTLRIQCDDGSITVNGIKMVNKKDVIYTNNGVINHLIDQVLIIPDSA  
 KQVIELAGKQOTTFTDEVAQLGLASALRPDGEYTLAPVINAFSDDTLSMDQELKLILQNHILKVKVGLNELY  
 NQQLILETIGGKQLRVFVYKTAVCIENTSCMEKGSQQRNGAINTFREILNPAEKSLEKGLKQDKRFEFTLSILEA  
 ADLKELLTFQGDWTLFVPTNDAFRGMTSEEKEILIRDKNALQHILLYHLTPGVFELGKGFEFGVTNHLTKTQGSK  
 ITLKEVNDTLVNLKASKESDIMTTNGVIVHVVDKLLYPADTPVGNDQLLELLNKLILKYIQTFVRGSTTFKEFTV  
 TVYRPTLTKVKLEGEPEFRILKEGRTITFEVINGEFTIKKYTKILDGVFVEITEKETREERLIIGPEIKITRIST  
 GGGETEETLKKLLQSEVTRVTKFTIEGGDGHLEFDEBEIKRLQGDTFVKLQANKKVQGSRRRLREGRSQ

**Signal sequence.**

amino acids 1-21

**N-glycosylation site.**

amino acids 599-602

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 507-510, 704-707

**N-myristoylation sites.**

amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,  
 476-481, 570-575, 741-746

**Fasciclin domains.**

amino acids 94-232, 234-367, 370-494, 496-630



129/162

**FIGURE 121**

MIFFLPMFSLLLLLVNFINANNHYDKILAH9PIGRDQGPNYCALQQILGTKKKYFSTCKINWYKKSICGQKTF  
 VINECPCPYMRMEGMKGPVAVLEIDHVGTLGIVGATTQRYSDA9KLBEEIBGKGSFTYFAPSNEANDNLSD  
 IRRGLASHNVNVELLHSLHSHMINKPMITKOLKNGMIIPSMYNNLGLFINHYPNGVVTVNCARIIGHNQIATNGV  
 VHYIDRVLTQIGTSIQGFIEREDDLSSTPRAAITSIDILEALGRDGHFTLFAPTNEAFEKLPQGVLERINGDKVA  
 SEALMKYHILNTLQCSSEINGGAVPETLRGHTIEIGCDGOSITVNGIKMVNKKOIVTNNGVILHIDQVLIIPDGA  
 KQVIELAGKQQTTFITDLVAQLGLASALRPDGEYTLAPVNNAFSDDTLSMDQLKLILQNHILKVKVGLNELY  
 NGQILETIGGKQLRVFPVYINTAVCIENSCMEKCSKQGRNGAIHIFREIIRPAERSLHEKIKQDRFSTFLSLLEA  
 ADLKEILLTQPGDWTLFPVTNDAFGMTSEKELLIPDKNALQMIILYHLTFPGVFPGKGFEPGVNTILKTTQGSK  
 IFLKEVNDTLLVNELEKESDIIMTTNGVIRVVDKILYPADTFVGNQQLLEILMKLIKTYIQIFVRGSTFKEIFV  
 TVYKPIKKYTKIIDGVPEITEKETREBKITITGPEIKYTRISTGGGSETLKKLLQEDTFVRKIQANKKVQG  
 SRRRLREGKRSQ

**Signal sequence.**

amino acids 1-21

**N-glycosylation site.**

amino acids 599-602

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 567-510, 674-677

**N-myristoylation sites.**
 amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,  
 476-481, 570-575, 711-716
**Fasciclin domains.**

amino acids 94-232, 234-367, 370-494, 496-630

130/162

**FIGURE 122**

NIFFLPMSFLLLLIVNFINANNHYKILANSRIRGRDQGFNVCAQCILGTKKKYFSTCKRWYKKSICQKKE  
 VLYECCPGYMRMBGKKGCPAVLEIDHVGTLGIVGATTQRYSDASKLRREIEGKGSFTYFAPSNEAWNLOSD  
 TRGLESNVAIVELLNALASHMINKPMITKDLKHGMIIPSMYNNLGLFINNYENGVTVMCAIILHGNQIATNGV  
 VHVVDVLTQIGTSIQDFIEREDOLSSFRAAAITSDILEALGRDGHFTLFAPTNEAEKLPQGVLERINGDKVA  
 SEALMKYHIINTLQCSESTIMGGAFTETLEGNTIEIGCDGDSITVNGIKMVNKKDIYTRNGVINLIDQVLIPOSA  
 KQVIELAGRQQTFTFDLVAQLGLASALAPDGEYTLAPVNNAFSDOTLSMDQPLKLLIQMHILKRVKVGINELY  
 NGQILETIGGKQKRVFVYRTAVCIENSCMEKGSQCGPNGAIHIFREIIEKFAEKSIMHEKLKQDKRFSTFLSLEEA  
 ADLKELLTQPDWTLFVPTNDRFKGMTSEEKILIRDKNALQNIILYZALTPGVFTGKGFEPGVNILEKTTQGSK  
 IFLKEVNDTLLVNELKSKESDIMEETNGVHVVDKLLYPADTFVGNDQLELILNKLKIKYIQKFFVKGSTFKEIPV  
 TVYRPTLTKVKIEGEPFRLIKEGETITSVINGEPIIKFYTRIIGVPEITEKETREERILTGPETKYTRIST  
 GGGETETLKKLLQEDTFVRKQLQANKKVQGSRRRLREGRSQ

**Signal sequence.**

amino acids 1-21

**N-glycosylation site.**

amino acids 599-602

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 507-510, 704-707

**N-myristoylation sites.**
 amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,  
 476-481, 570-575, 741-746
**Fasciadin domains.**

amino acids 94-232, 234-367, 370-494, 496-630

131/162

**FIGURE 123**

NIFFFLPMFSLDLLLVNPNINAMHYDKLLAHSRIQRDQGPVNCALQQILGTKKKYPSTCKNWKKSICGQKTT  
 VLYECCPQYNNRMGKMGCPAVLFYDHYVGTGLGVGATTTQRYSDASKLREEIEGROSTTYFAPSNEAWDHLUSD  
 IRRGLESNNVVELLNALSHSMINKRMETKDLKNGMIIPSMYNNLGLFINHYPNGVVTVNCARLIHGNQIATNGV  
 VHVIDRVLTQIGTSIQDEIEADDLSFFKARATTSUILEALGRDGHFTLFAPTNEAFKELFRGVLERIMQDKVA  
 SEALNKYHILNTLQCSSEIMCGAVFETLEGHTIETGCDGDSITVNGIKMVNKKGIIVTNNGVTHLIDQVLIQDSA  
 KQVIELAGKQQTFTTDLVAQLGLASALRPGGEYTLAPVNNASUOTLSMDQRLKLLQNHILKVKVGLNELY  
 NGQILLETIGGKQLFVYVYRTAVCTIENSCMEKSGSKGSRNGAIHIFREIIPAEKSLREKLRQKKRSTFLSLLER  
 ADLKELLTQPGDWTLFVPTNDAPKGMFSREKELLRLDKNALQNIILYHLTPGVFTGKGFEPGVYTNILKTTQSGK  
 LFLAEVNDTLVNLKSKESDINTTNGVHVVDKLLYPADTFVGNQDQLEILNKLINVIQIKFVFGSTFKETIPV  
 TVYKPIIKKYTKIIDGVPEITEKETAREEIIITGPEIKYTRISTGGGTEETLKLKLQEEVTVKTKFLEGGDGH  
 LEEDDEIRLLQGGTTPVRKLQANKKVQSSRRRLREGRGQ

**Signal sequence.**

amino acids 1-21

**N-glycosylation site.**

amino acids 599-602

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 507-510, 674-677

**N-myristoylation sites.**
 amino acids 70-75, 106-111, 109-114, 152-157, 193-198, 214-219, 392-397,  
 476-481, 570-575, 711-716
**Fasciclin domains.**

amino acids 94-232, 234-367, 370-494, 496-630

132/162

**FIGURE 124**

MVNYAMAGPSQRKILWRSVAVLTCKSQVVRPGYRGGLGARRSTLLKTCARARATAPGAMKMWAEPTRFYSHSCCL  
CCNVFTGTLILGVWYLIINAVVLILLCLADPDQYNFSSSELGGDFEFMDAMMCIAFAISLLMILICAMATY  
GNYKQRAAWIIPFFCYQLDFALNHLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPCTCLVLIILLFISII  
LTFKGYLLSCVMHCYRYINGRNSSDVLVYVTENDTTVLLPPYDDATVNGAAKEPPFPYVSA

**Transmembrane domains.**

amino acids 83-103, 124-144, 162-182, 205-225

**N-glycosylation sites.**

amino acids 111-114, 244-227, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 39-42

**Tyrosine kinase phosphorylation site.**

amino acids 243-251

**N-myristoylation site.**

amino acids 34-39

133/162

**FIGURE 125**

MPGQGGGLQARRSTILKTCARAKATAPGAMMMVAPWTRFYNSCCICCHVKTGILLGVWYLIINAVLLILLSA  
LADPDQYNFSSSELGGDFEFMDANMCIAIATISLLAILICAMATYGAIRQRARMILPFCYQLFDFALNMVAI  
TVLIYFNSIQEYIRQLPPNFFYRDDVMSVNPFCVLVLIILLFISILLFEGYLISCVMNCYRYINGPSSDVLVY  
VTENDTTVLLPFYDDATVNGRAKEFFFPFYVSA

**Transmembrane domains.**

amino acids 54-74, 95-115, 133-153, 176-196

**N-glycosylation sites.**

amino acids 82-85, 215-218, 226-229

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 10-13

**Tyrosine kinase phosphorylation site.**

amino acids 214-222

**N-myristoylation site.**

amino acids 5-10

134/162

**FIGURE 126**

MGRAGGGGFGPGFPFLLFLGALVLASGAVPAREAGSAVEAEELVKGSFPAWEFPANDTREAGFFAAGEDEAS  
 WTAPGGELAGPSEVILQESAIVTGTAWLEADSPGLGGVTAEAGSGDAQALPATLQAPHEVLGQSIMPPIPRATE  
 ASGFPSPFTPGDKLSASELPKESPLEVWMLGGSTPDPQVPELTYPFGTLEFPQASDTIDIDYFEGELGEGNG  
 ADLGSFPSPGTSSENHPDTEGETPFWNSLLDLYDDFTTFDESDFYPTTSFYDOLDEEEEEEDDKDAVGGGULED  
 ENELLYPTGKPGGLPGCTGQPTSPWHAVPPQHTLGSVPSSIALRPRPGEPRGRDLASSENGETCFPSGFFVRNGSC  
 RSVCDLFPSPYCHNNGGCYLVENIGAPPCRCNTQDYINRKGMRCEIITDFQVMCVAVGSAALVLLLLFMFTVFFA  
 KKLVLKLTENTKLRRTNKPRTPSELENDNFBLSLIAEGSHFNDDPSAPHKIQEVLKSKLKEESFNIGNMSPK  
 LEGGEGEGADLDVFCLOHILT

**Signal sequence.**

amino acids 1-30

**Transmembrane domain.**

amino acids 423-443

**N-glycosylation sites.**

amino acids 57-60, 355-358, 367-370, 473-476

**N-myristoylation sites.**
 amino acids 6-11, 29-34, 79-84, 109-114, 116-121, 222-227, 226-231, 230-235,  
 233-238, 308-313, 314-319, 330-335, 334-339, 368-373, 482-487

135/162

**FIGURE 127**

MLPVYQEVKPIPLQDANICSRVFFWMLNELFKIGKRPLREDIMYSVLPEDRSQHLGSEELGGTFWDKCEYLRAEND  
 AQKPSLTBALIKCYWKSYLEVLGFTLIRESAKVIQPIFLGKIINYFENYDPMOSVALNTAYATVLPFCTLLIL  
 AILSHLYFYHVCQGMRLVAMCHNTRYKALRLSNMAMSKITPGQIVNLLSNDVNKFDQVTVPLHFLRAGFLQA  
 IAVTALLWMEIGITSCLAGMAVLIILLPLQSCFGKLFSSLSRSTATTUARIIRTMNEVITGIRILKMYANEKSSFS  
 NLITNLAKKELSKILRSSCLRGMLASFFSASNTIVYVFTTYVVLGSEVTHASRVFVAVTVLYGAVELFTVLEFPF  
 SAIERVSEAVTVSIRIQTFLLLDEITSQANRQLPSDGKKMVRVQDFTAFWOKASETPTLLQGLSFTVRKPELLAVV  
 GPFVQAKGSELSLAVLDELAPSHGLVSVHGRIAYVSQGFVWVPSCTLASNILPGKKYKERYEKVIKACALKKDLQ  
 LLEDGDLTVIGDRGTTLSGGQKARVNLARAVYQDADILLLDDPLSAVDAEVSHPHFLCICQLLRKIKITILVTR  
 QLQYLKAASQILILKDGKRMVQKGTYTEFLKSGIDFGSLKKONEESQPPVFGTPTLNRNPTSESSVMSQQSSN  
 PSLRGDALESQDTENVFVTLSEENRSEGGKVGFCAYKNYFRAGAHNIVFTPLILNTARQVAVVLDQNWLSYWAN  
 KQSMLEAVTVNGGGNVTEKLULNWLGLYSGLTVATVLPGLIARSLLEVYVLVNSSQLLANKMFESILKAPVLFED  
 RNPICGRILRRFSKDIGHLDLPLTFLDFIQTLQVVGVSVAVAVIPWIALPLVPLGLIIFILFRYFLETSRD  
 VKRLSTTSQVVFHLSSELQGLWTIRAYKAEKRCQELFQAHQLHSEAWFLFTTSKWFVAVRLDAICAMFVII  
 VAFGSELLAKTLDAQVGLALSYALTLMGFMQMCVQSAEVENMISVERVIEYTOLEKEAPWYQKKEPPFAMP  
 HEGVLIIDNVNFMYSGGGLVLKHLTALIKSQEKVQIVGRGTACKSSILSALFPLESEEGKINWIDKILITTEIGL  
 HOLRKKMSITPQEPVLTFTGMPKHLDPFKESHTDEELWNLQEVQLKETIEDLPCKMCTELAESGNSFSVQGRQL  
 VCLARALIRKNGILTIIDENATANVDPTDELIOKKIREFAHCTVLTIAHRINTIIDSCKIMVLDSGRLEYDEP  
 YVLLQNKESLKYKVVQQLGRKAAALLETAKQVYFKNYPHIGHTDMMVTNTSNGQFSTLITFTAL

**Transmembrane domains:**

amino acids 134-154, 233-253, 346-366, 708-728, 767-787, 834-854, 857-877,  
 948-968, 967-987

**N-glycosylation sites.**

amino acids 651-654, 690-693, 746-749, 754-757, 792-795, 1176-1179, 1309-1312

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 1115-1118

**Tyrosine kinase phosphorylation sites.**

amino acids 37-45, 497-504, 1253-1259

**N-myristoylation sites.**

amino acids 192-197, 318-323, 343-346, 430-435, 448-453, 487-492, 532-537,  
 537-542, 624-629, 672-677, 752-575, 766-771, 770-775, 779-784, 980-985,  
 1078-1083, 1174-1179, 1313-1318

**Amidation sites.**

amino acids 405-410, 495-500

**ATP/GTP-binding site motif A (P-loop).**

amino acids 445-452, 1075-1082

**AEC transporter.**

amino acids 438-609, 1068-1250

**AEC transporter transmembrane region.**

amino acids 92-365, 711-997

136/162

**FIGURE 128**

MSALRRKFGDDYQVVTSSSGSGLQFGGFGQQLVPKKGRQRFVDKNGRNVQHGNLGSSTSRXLSDLFTT  
LVQLKWRNNLFIETTYTVAWLEMASMWWVIAYTRGDLNKAHVGHYTPCVANVYNFPSAFLFTIETATIGYGY  
RYITDKCPFGILLFLFQSTILGSIVDAFILGCMFIRKSGPKKRAETLMFSENAVLSMRDGKLTIMPRVGNLNSH  
MVSQIECKLLKSRQTFEGSEFLDQLLELDVGFSTGRDQLFLVSEPLTICHVIDAKSPFYDLSQRSWQTEQPRIV  
VILEGIVETTGMTQQRATSYTEDEVLMGHRFFFPVIGLEEGTFKVDYSQFHATFEVFTPPYSVKEQEMLLMSSP  
LIAFAITNSKERHNSVECLDGLDUTTKLPKSLQKITGREDFFPKLLRMSSTTSEKAYSLGDLNKLQKISSVF  
GNSEKILVSKTTKMLSLDMSQSVADLFPKIQKMGAGGARMEGNLPKALKRKMMSDPT

**Transmembrane domains.**

amino acids 83-103, 120-140, 158-178

**Glycosaminoglycan attachment site.**

amino acids 26-23

**N-myristoylation sites.**

amino acids 58-63, 61-66, 216-221, 301-306, 486-491

**Cell attachment sequence.**

amino acids 109-114

**Inward rectifier potassium channel.**

amino acids 47-393



137/162

**FIGURE 129**

MFLFKNTSVSSLYSGCRLLLRPEKDGAAATRVDAVCTHRPDKSPGLDREKLYNKLSQLTHGITELGPPYTLDRR  
 SLYVNGFTAQSSMTTKTETDSTIMHLATSRTEASLSGPTTASPLLVLTINFTITNLRYENNHRPGRKKNFT  
 ERVLQGLLRPFYKNTSVGPLYSGCRLLLRPEKDGAAATKVDICTYRPDPKSPGLDRQQLYWELESQSLNFTITEL  
 GPYTLDRDSLYVNGFTQSSVPTTSDIETPTVDLGTSGTFVSKFGPDAASPLLVLTINFTITNLRYENNHRPGRKKNFT  
 GSRKKNFTTFRVLQGLLRSLPKSTSVGPLYSGCRLLLRPEKDGATGVDICTHRPDPKSPGLDRQQLYWELESQ  
 LTHNFTITELGHYALDNDSLFVNGFTHRSSVPTTSTPTPTVYLGAASKTEASIEGSPDAASHLILFTINFTITNL  
 RYENNHRPGRKKNFTTFRVLQGLLRPLPKNTSVGPLYSGSRLLLRPEKDGATGVDICTHRPDPKSPGLDRQ  
 QLYWELESQSLNFTITELGPYTLDRDSLYVNGFTHRSSVPTTSTGTVSEEPFTINFTITNLRYENNHRPGRKKNFT  
 TDHVMKHLRSLPLFQRSSIGARYTCKRVIALRSVKNGAATRVVLLCTYQLPLSGFGLPIKQVFEHLSQQTGGRITR  
 LGPYSLDKDSLILNGYNEPGLDEPPTTPKPTATPLPLPLSEATTAMGYRLKTLTINFTITNLRYENNHRPGRKKNFT  
 NSTEGVLQHLRLPLFQRSSMGFFYLGCQLISLRPEKDGATGVDICTYRPDPKSPGLDRQQLYWELESQSLTHGV  
 TQLGTYVLDNRDSLFINGYAPQNLISIRGEYQINFIHVMNLSNPDFTSSHYITLLRDLQKVTTLXGSQLHUTF  
 RPLVLTALTMDSVIVTKALFSSNLDPSLVEQVPLDKTLNRSFHWLGSYQLVNDIHTVTHRESSVYQPTSSSSSTQ  
 HTYPTFTITNLRYENNHRPGRKKNFTTFRVLQGLLRSLPKSTSVGPLYSGCRLLLRPEKDGATGVDICTHRPDPKSPGLDRQ  
 SPLAKRVDRVAIYEFLEMTTRNGTQLQNFELDRSSVLYDGYSPMRNEPLTONSDLPFWAVIFIGLAGLGLITC  
 LIGCVLTITARRKKEGEYNVQQCPGYYSQSLDLEDLQ

**Transmembrane domains.**

amino acids 107-127, 418-438, 1093-1113

**N-glycosylation sites.**

amino acids 6-9, 125-128, 146-149, 162-165, 281-284, 302-305, 374-377,  
 385-388, 437-440, 457-460, 473-476, 570-573, 591-594, 721-724, 741-744,  
 836-838, 853-856, 895-898, 928-931, 967-970, 1004-1007, 1058-1061, 1064-1067

**Glycosaminoglycan attachment site.**

amino acids 644-647

**Tyrosine kinase phosphorylation sites.**

amino acids 358-365, 1121-1129

**N-myristoylation sites.**

amino acids 15-20, 171-176, 260-265, 310-315, 327-332, 339-344, 482-487,  
 583-586, 611-616, 778-783, 782-787, 1106-1111, 1114-1119

**SEA domain.**

amino acids 112-245, 270-391, 661-684

138/162

**FIGURE 130**

MGNWVYVNHVSVLFLVYVWIGLVFLFVDAFLKYERADKYTYTRKILGSTLACARASALCINFNSTLILLPVCRN  
 LLSFLRGTCISFCSTFLRKQLDHLTFHKL VAYMICLPTAII IAHLEWFDCCYSRSRQATDQSLASILSSLSHDE  
 RKGGSWLNPIQSRTTFVEYVTFPSVAGLTGVIMTLALILMVTSATEFIRRSYFVFWYTHHLTFIFYILGLGLNG  
 IGGIYVPGQTESMESHPRKCAESFEMNDDRDSDRCRRPKFEGHPPESWKILAPVILYTCERILRFRSQQKV  
 ITKVVMHPSKVLELQNNKNGFSMEVGQYIFVNCPSISLLEWHFFTLTSAPSEDFFSIHIPAGDWTENLIRAF  
 QQYSPFIPRIEVDGFFGTASEDVFQYEVAVLVGAGIGVTFPASILKSINWYKFCADHNLTKKTIYFWICRETGA  
 FSWFWNLLTSLEQEMELGXVGLNRYRLFITGWGDSNIVGHAALNFDKATDIVTGLKQKTSFGPMMWNEFSTIA  
 TSHPKSVVGVFLCGPRTLRKSLRKCCRFYSSLDPRKVQFYFNKNEF

**Signal sequence.**

amino acids 1-29

**Transmembrane domain.**

amino acids 44-64, 60-80, 99-119, 168-188, 204-224

**N-glycosylation sites.**

amino acids 63-66, 97-100, 162-165, 236-239

**Tyrosine kinase phosphorylation sites.**

amino acids 198-206, 367-373

**N-myristoylation sites.**

amino acids 47-62, 135-140, 178-183, 225-230, 402-407, 527-532

**Ferric reductase like.**

amino acids 46-563

139/162

**FIGURE 131**

MGNWVVRNRFVSFLFLVVLGLNVFLFVDAFLKYEKADKYYTTRKILGSTLACARASALCLNFNSTLILPVCRN  
 LLSEFLRGTCSCFCSNLTFRKQLDHNLTPHKLVAYMICLWTATHTTAHLENFDCYGRSRQATDGSIASTLSLSHDE  
 KKGGSWLNPIQSRNTTVEVVTFTSIAGLTGVIMTIALILMVTGATEFIRRSYFEVFWYTHLSFIIFYILGLGIAG  
 TGGTVRGQTEESMNEHSHPRKCAESFEMWDDRDSDHCRPRKFEGRHPPESWKKILAPVILYICERILRFYPSQQKVV  
 FTKVMSPECKVLELQMNKRGSMEVGQYIFVNCPSISLEWHFFTLTSAFEEDFTSIRRAAGWTENLIRATE  
 QQYSPIFRIEVDGPFGTASEDVQYEVAVLVGAIGVTPFASILKSIWYKFKQCADHNLKTKKIYFYNICKETGA  
 FSWFNHLLTSLQEMEEELGKVGFLMYRLFLTGWDSNIVGHARLNFQKATCDIVTGLKQKTSFGRPMWWDNEFTIA  
 TSHPKSVVGVFLCGERTLAKSLRKCCARYSSLDPRKVQYIFNKENT

**Transmembrane domains.**

amino acids 6-26, 44-64, 60-60, 99-119, 168-188, 204-224

**N-glycosylation sites.**

amino acids 63-66, 97-100, 162-165, 236-239

**Tyrosine kinase phosphorylation sites.**

amino acids 198-206, 367-373

**N-myristoylation sites.**

amino acids 47-52, 135-140, 178-183, 225-230, 402-407, 527-532

**Ferric reductase like transmembrane.**

amino acids 46-563

140/162

**FIGURE 132**

MGNWVYNHWFSVLFLVVWLGDNVFLFVDAFLKYERADKTYTYTRKILGSKWKLAPVILYICENILRFYRSQQKV  
VITKVVMMHPSKVLELQMKRGFSMEVQYI FVMCPSTSLLEWHFFTLTSAPERDFTSIHIRAGDWTENLIRAF  
EQQYSPIPIRIEVDGPFCTASEEVFPQYEVAVLVGAGIGVTPTASILKSIWYKFQCADHNLTKKVGHAALLNFDKA  
TDIVTGLKQETSEGRPMWDMNEFSTIATSHPKSVVGVFLLCGPRTLAKBLRKCHRYSSLDPKRVQFYFNKENFO

**Transmembrane domains.**

amino acids 6-26, 44-64

**Tyrosine kinase phosphorylation site.**

amino acids 146-152

**N-myristoylation sites.**

amino acids 181-186, 257-262

**Ferric reductase like transmembrane.**

amino acids 1-293

141/162

**FIGURE 133**

MGNWVVNANFVSFLVVLGLNVFLFVDAFLKTEKADRYYYTRKILGSTLACARASALCLNFNSTLLLPVCRN  
 LLSFLRGTCSECSKRLAKQLDNLIFBKGLVAYMICLHTAIHIIAHLTFNFDYSRSGQATDGLASILSSLSRDE  
 KRGGSWLHPIQSRNTTVEYVFTFSIAGITGVIMTIALILMVTSAFERIRRSYFEVFWYTHHLFTFYILGLGING  
 IGGTIVGGQTEESMNESHPRKCAESFEMWDDRDSHCRRPKFEGHPPESSHWILAPVILYICERILRFYRSQQKV  
 ITHVVMHPSVLELQMNKRGFSMEVGQYIFVNCFTISLEWHFFTITSAPESDFFSIRIRAAQDWTENIRAFE  
 QQXSPFPIRIVEVGGFFGTASSDVFQYEVAVLVGAGIGVTFPASILKSIWYKFCQADHNLKTKKVGHAAINFDKAT  
 DIVTGLKQKTSFGRPMNDNEFSTIATSHPKSVVGVFLCGPRTLAKSLRKCCHRYSSELDPRKVQFYFNKENF

**Transmembrane domains.**

amino acids 6-26, 44-64, 60-80, 99-119, 168-188, 204-224

**N-glycosylation sites.**

amino acids 63-66, 97-100, 162-165, 236-239

**Tyrosine kinase phosphorylation sites.**

amino acids 198-206, 367-373

**N-myristoylation sites.**

amino acids 47-52, 135-140, 176-183, 225-230, 402-407, 478-483

**Ferric reductase like transmembrane.**

amino acids 46-514

142/162

**FIGURE 134**

MTSGSVFFYILIFGKYFSHGGGQDVKCSLSGYFFCSNITKCLPQLLHCNGVDDCGNQADEDCGDNHGWNSQDFK  
 YFASYYKMTSQYFFEAEETPECLVGSVPVQCQCQGLELCCDETNLRAPVSVSSNVTSMSLQWNLIRKLPDPDFKN  
 YKDLQKLYLQNNKITSISTYAFRGLMSLTXLYLSHNRITFLKPGVFEDLHKLWLIIDNNHLSRTGPTTFYGLN  
 SLTLVLWNNVITRLPDKPLCQHMPRLHWLDLEGNNHINLRNLTFISCSNLTVLNMRKNKINNHNMENTTAPLQK  
 LDELGLGNNKTNLPLPLFKDLKELSGENLSYNPIQNTQANQFDYLYKLSLSLEGITETSNIQRMFRPLMNL  
 SYFKKPKYQCYGAPHYRSCPKNTDGISSLENLLASIIQRVFWVVSATVCPGNLFVICHMRPYIRSENKLYAMSI  
 ISLACADCLMGYILFVIGGFDLNRFGYNNKHAQLWMSETHCQLVGSIALI9TEVSVLLITFLTKYICIVYFF  
 RCVRPAGKORTITVILILWITGFLVAFIPLSNKEFFKNVYGTNGVCFFLHSEDTESIGAQIYSVAIFLGINLAIF  
 IIVFSYGSNMFYSVHQSAITATELRNQVKKEMILAKRFFPIVFTDALCNIPFVVKFLSLQLQVEIFGTITSWVV  
 IFILPINSALWPILYITLTTPFKEMIHRFWINYRQRKMDSKQKTYAPSVIWWZMWFLQEMPELAKRFDLFTY  
 PCMSLISQSTRNLNSYS

**Transmembrane domains.**

amino acids 212-232, 404-424, 443-453, 489-509, 526-546, 577-597, 629-649,  
 665-685

**N-glycosylation sites.**

amino acids 36-39, 127-130, 264-267, 272-275, 325-328, 368-371

**N-myristoylation sites.**

amino acids 49-54, 352-357, 586-591, 659-664

**Leucine zipper pattern.**

amino acids 487-508

**LDL-receptor class A.**

amino acids 40-59

**G-protein coupled receptor.**

amino acids 159-189, 413-432, 422-452, 436-466, 478-518, 528-547, 625-644,  
 673-689

**Leucine rich repeats.**

amino acids 127-150, 151-174, 175-196, 196-222, 223-246, 248-271, 272-295,  
 296-319, 320-343, 344-367

**7 transmembrane receptor (rhodopsin family proteins).**

amino acids 485-681

**Low-density lipoprotein receptor domain.**

amino acids 25-64

143/162

# FIGURE 135

MTSGSVFFYILIFGKYFSHSGGQDVKCSLGYFPCGNITTKCLPQLLRCHGVDDCGNQADEHCGGDNNGWSLQPK  
YFASYYKMTSQYPPFARTEPECLVGSVPVQCLCQGLELDCEDETNLSAVPSVSSNVTAMSLQWNILRKLPDCKN  
YHDLQKLYLQNHKITSLSIYAFRGLNSLTCLYLSHNRTITFLKPGVFEDLHRLENLITEDNHLBRISPTTFYGLN  
SLILLVLMNNVITFLPKPLCQHMERLHWLEGNHINHLRNLTFISCSNLTIVLVMRENKINHLMENTFAPLQK  
LDELQGLSNKIENLFPFLIFDKLELSQLNLSVNF IQKIQARQFDYLVKLSLSLEGIEISNIQORMFRPLMNSI  
HIYFKKFQYCGYAPHVRSCKPHFDGIBSLENILLASLIQRFVFWVVSAYTCFQNI FVICMRPYIRSENKLYAMSI  
ISLCCADCIMGIYLFVIGGFDLKFFGGEYNKHAQLMMESTHCQLVGSLLISTEVSULLTFLTEKYICIVYFF  
RCVRPGKCRITITVILILINWITGRIVAFIPLSNKEFFKNXYGTNGVCFFLESEDESIGAQIYSVAIFLGINLAAF  
ITIVFSYGSMEYSVHGSAITATEIRNQVKEMILAKREFFIVETDALCNIPIFVVKFLSLQVETPGTITSWVV  
IFILPINSALNFILYTLTTRPFKEMLARFWYNYRQRKQMDSKGQKTYPARSPINWEMVPLQMPPELAKPDFTY  
PCEMSLISQSTRINSYS

## **Transmembrane domains.**

amino acids 212-232, 404-424, 443-463, 489-509, 526-546, 577-597, 629-649,  
665-685

## **N-glycosylation sites.**

amino acids 36-39, 127-130, 264-267, 272-275, 325-328, 368-371

## **N-myristoylation sites.**

amino acids 49-54, 352-357, 586-591, 659-664

## **Leucine zipper pattern.**

amino acids 487-508

## **Leucine rich repeats.**

amino acids 127-150, 151-174, 175-198, 199-222, 223-246, 248-271, 272-295,  
296-319, 320-343, 344-367

## **7 transmembrane receptor (rhodopsin family).**

amino acids 59-259

## **Low-density lipoprotein receptor domain.**

amino acids 25-64

144/162

**FIGURE 136**

MGRILASRPLLLALLSLALCRGRVVRVPTATLVRVVGTELVI PCNVSDYDGPSEQNFQWSFSSLSGSFVELASTW  
 EVGFAQLYQERLQAGSTILLRRTANDAVELALKNVQPSDQGHYKCSPTSIDATVQGNVEDTVQVHLADSLAVG  
 PGAPPPPSLSIREQEPFELLECTAASASPLHTLALLWVVRGPARBSVLALTBGRPHPLGYEQRYHSGDVRLL  
 DTVGSDAYRLSVSRALSDAQSGSYRCIVSEWIAEQGNMQETQEKAVFVATVVIIQPTVLRAAVPKNVSVAEGEELD  
 LTCNITTDRADDVRPEVENGFSRMPDSTLPGSRVRLARLDRDSLHSSSPHVALSHVDARSYHLLVRDVSKEGXY  
 YYCHVSLWAPGNRSHKVAEAVSSPAGVGVTWLEPDYQVYLNASKVPGFADDPTLACRVVDTKSGEANVRFT  
 VSNYIYMNRRSDNVVTSELLAVMDGDTLKYGERSKORADGDFITSKEHTDTNFRIQRTTEEDRGNYVCVVS  
 AWTQQRNNSNVKSDVFSKPVNITWALEDSVLVVKARQPKPTFAAGHTFMTCKVSSKNIRSFYSVLIMAEKF  
 VGULSSPMETKYIISLDQDSVVKLENWTDASRYDGVVLEKVVQDEFRYRMYQTQVSDAGLYRCMVTAWSFVRGS  
 LWKEAATSLSNFIEDFTQTBGPIFNASVHSDTPSVIRGDLIKLFCITTEVEGAALDDDDMAFDVSWFAVBSFGLD  
 KAPVLLSSLDKRGIVTTSRRDWKSDLSLERVSVLEPLLQVHGSEDQDFGNYYCSVTPWVKSPPTGSSWQKEAELHS  
 KPVFITVMQVILNAPKYPELLIGIGLSTVIGLLSLIGYCS9HWCCKKEVQETTRREKKRLMSMEMD

**Signal sequence.**

amino acids 1-21

**Transmembrane domain.**

amino acids 833-853

**N-glycosylation sites.**
 amino acids 44-47, 286-289, 300-303, 383-386, 413-416, 525-528, 600-603,  
 618-621, 631-634
**Tyrosine kinase phosphorylation site.**

amino acids 632-640

**N-myristoylation sites.**
 amino acids 243-248, 398-403, 511-516, 651-656, 753-758, 789-794, 836-841,  
 844-849
**Cell attachment sequence.**

amino acids 703-705

**Immunoglobulin domain.**

amino acids 36-121, 162-249, 292-375, 422-517, 564-657, 704-795



145/162

**FIGURE 137**

MSRSRLGKIRKRLLEUVKSKNVEPARADFSDNESARLATLALLDGGGEAYWRVLSQEGEYDFLSSVEAQYIQAG  
AREPPCPPTFLGGAEAGPKGLDSSSLQSGTYFFVASGGSEYALLNSWASAEKPYLKEKBSATYYFQTVKHNHNR  
DLVRRICITRTSQVLVILMDVFTQVEIFCDILEPANKRGVFCVLLDQGGVKLEQEMCDKVQIQSDSHKNNISIRS  
VEGEIYCAKSGRKFAQQIREKFIISDWRFVLGGSYSFNTLCGHVHNNILSKFTGQAVELPDEEFHLYASSKPV  
MGLKSPRLVAPVPPGAAPANGRLSSGSGGASDRTSSNPFSGRSGSHPTRESVSASSGPGSPAPHPFPFPPFPFQ  
PHQGGPWGAFFSPQRLSPFPHDGPAAVYSNLGAYKPTLQLEQLGLVERLTPTWRPPLQASPHF

**Transmembrane domain.**

amino acids 154-175

**N-glycosylation sites.**

amino acids 32-35, 217-220

**Tyrosine kinase phosphorylation site.**

amino acids 221-228

**N-myristoylation sites.**

amino acids 45-55, 86-91, 94-99, 112-117, 186-191, 311-316, 341-346

**Amidation site.**

amino acids 232-235

146/162

**FIGURE 138**

NALPQPPPPAGARCPVTPEW#ASGPPSQAPLLRQEAKEEEEGESTGVQGANCTGTAEQRRRCHGEAAESAAAE  
 EQQAEEVGGAAAAGSGSPAGGAGGGGLGSWRPLLAWLQRHQPCQCPCAAFLGRSAAHCCCHGGTMAALAYNLGRRE  
 INHYFQVPSAKVLALVAYLLLAACHLASRAYRGNDSCETLLSSGPFLEKQVWQFHSMMHVFYKISEAKNCLVDK  
 HIAFIGDSRIQLFYSFVKIINPQFKBEGNKHENIPFEDKTLASVKVDPLMHFEVNGSMKQCINVTEDSIAKPH  
 VTVAGAAWTSIKIRNGSSEALSQYRMNITSIAPLELLEKLAKTSUVYVWLQDPVIEDLLSEHAKMITNERTIDAYNE  
 AAVSIINSSTRNSKSNVENFVSUKLIAGETIMESLDGLHLEESSPETTAMLLNNVYCNKLLKFPDGGSCCQPRFP  
 VTLLQKLAACTFFLSTIGYLIFYIIHUNAHRKKNKPCOTULESGEERKNIIINTPVSSLEILLQSFCKLGLIMAYFY  
 MCDRANLFWKENKFYTHSSFFIPIIYLLVLAGVYMENTKRTKVLAREQTDSEWKNMQLVILIYRLSGASTFLEV  
 YMHRLVLVAAYLFQTFYGHFSYFWIKGDFGIYRVCQVLFRLNLFVVLICIVMDRFYQFYFYFVPLTVYMFVLYV  
 TLALWFOQLIQKAWGNCFWHEGLDLKGLLLFTCFLAYSQGAEETIFSLWPLSKCPKELKGNVYEWNRMRDR  
 YVVFHGLMFAFYLLALQKRQILSEGEKEPLFSNKNISNELLFTISVVSFLEYSIWASSCKNKAECNELHFEVSVVQ  
 ILAFILTRNIPGYAPSVYSSFFAWFGKISLELEFCQXHINLAADTRGILVLIPGRFMLNIIVSTFTFVCVAHET  
 SQITNDLAQIIIPKDNSSLLKRLACIAAFFCGLLILLSSIQDKSKH

**Transmembrane domains.**

amino acids 153-173, 447-467, 495-515, 532-552, 577-597, 624-644, 651-671,  
 677-697, 693-713, 733-753, 771-791, 808-828, 866-886, 904-924

**N-glycosylation sites.**

amino acids 182-185, 277-280, 311-314, 323-326, 377-380, 904-907

**Tyrosine kinase phosphorylation site.**

amino acids 180-187

**N-myristoylation sites.**

amino acids 47-52, 50-55, 53-58, 81-86, 82-87, 89-94, 93-98, 94-99, 96-101,  
 97-102, 134-139, 181-186, 312-317, 511-516, 549-554, 746-751

**Amidation site.**

amino acids 144-147

147/162

**FIGURE 139**

MYHCHSGSKPTEKQANETAYAKWKLCSASAICFIFMTAEVVGSHAGSLAVVETDAAHLLIDLTSEFLSLFSLWL  
SSKPPSKRLTFGWHRAEILGALLSILCTINVTGVLVYIACERLLYPDYQIQATVMIIVSSCAVAANIVLTIVVLH  
QRCLGWHNKEVQANASVRAEFVHALGDLFQSISVLISALITYKFEYKIADPTCTFIFSTILVLAATITILKDFS  
ILLMEGVFKSLNYSGVKELILAVUGVLSVHSLHWSLTNNQVILSAHVNTAASRDSQVVKRELAKALSKSFTMR  
SLTIQMESPVDQDPCLFCEDPCD

**Transmembrane domains.**

amino acids 53-73, 91-111, 127-147, 166-186, 202-222

**N-glycosylation sites.**

amino acids 162-165, 234-237

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 81-84

**Tyrosine kinase phosphorylation site.**

amino acids 13-20

**N-myristoylation sites.**

amino acids 7-12, 42-47, 94-99, 228-233

**Cation efflux family.**

amino acids 78-306

148/162

**FIGURE 140**

MVLSVFVIALGATLGTNTSILALCGVTCLCRHMPKKGLLPDQDPLEKAKPSILGSAQQFNVKKSTEPVQPR  
ALLKFPDIYGPRAVTAPEVINYADYSLRSTERTAPASQPPND SRLKRQVTEELFILPQNGVVEDVCVMTW  
NPEKAASWNQAPKLYCLOYDQCMAELFVTRLEAVTSNHGGCCCYVQGSVANRTGVSVEAQTALAKRQLHTTNE  
EGLVLP LAEEEELEPTATLTLTLCODRFSRHSVAGELRLGLDGTSVFLAAATWGLKTSAKEPSAGAGEVILGIS  
YLEAANRLLVVLIKANMLHSNQSKELLGKDVSVKVTCLKHQARKLKKRQTERAKRKRINFVNNEMIFELPDALLQ  
ASSVREVLQQDDSQSCALSHCSLGLHTSGSERSHWEEMLKNPRRQIAMWHQLHL

**Signal sequence.**

amino acids 1-24

**Transmembrane domain.**

amino acids 4-24

**N-glycosylation sites.**

amino acids 118-121, 201-204, 317-320

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 65-68, 342-345

**N-myristoylation sites.**amino acids 11-16, 15-20, 189-194, 197-202, 204-209, 261-266, 380-385,  
385-390, 396-401, 401-406**C2 domain.**

amino acids 304-394

149/162

**FIGURE 141**

MQKIMHSIVLLSPVLWGLIFGVSSNSIQIGGLEPRGADQEYSAFRVGMVQFSTSEFR/LPHIDMLEVANSFAVT  
NAFCSQPSKGVYAI PGFYDEKSVNTITSPCGTLHVSFLTPSPFTDGT HPFVIQMRPDLKGA LLSLEYVQWQKF  
AYLYDSDRGSLSTIQAVLDSAAKKKMQVTAINVGNINNDKKDEMYRALEFQDLKKKRRVILDCERDKVNDIVDQ  
VITIGKEHVKGYYITIANLEPTDADLLKIQFGGANVSGFQIVDYDDSLVSKFIERNSTLEEKEYPGAHTTTAKVT  
SALEYDADVQVMTAFRNLIRKQPIETSRDGNAGDCLANPAVFWQGVETIERALQVQVEGLSONIKFDQNGKRIN  
YTNIMELKTNKPRKIGYVSEVDMVVLTELPSCNDTSGLENKTVVVTFILESPYVMKKNHMELEGNERYEG  
YCVDLAAETAKHSGFKYKLTIVGDGKYGARDADTKIWNMGVGLVYKADIAIAPLTITTLVREEVIDFSKPTMG  
LGISIMIKKPKSKPGVFSFLDPLATEIWMCI VEAYIGVSVVLFLVSRFSPYEWHTTEFDGRETQSSKSTNEF  
GIFNLSLWFSLGAFMRQGC DISPRSLSGRIVGGVWFFTLILISSYTANLA AFLTVERMVSPIESBEDLSKQTEI  
AVGTLDSGSKTEFFRFSKIAVEDKMTYMRSAE PSVEVRRTAEGVARVRKSKGYAYLLESTNNEYIEQKPCD  
TMKVGGRLDSKGYGIATPKGSSLGTPVNLAVLKLSEQGVLDKLNKQWYDKGECQAKDSSGSKERTSALSLSNVA  
GVFYILVGGGLGLAMIVALIEFCYKSRAEAKPMKVAKNAQNINPSSSQNSQNFATYKEGYNVVYGLSEVKI

**Signal sequence.**

amino acids 1-21

**Transmembrane domains.**

amino acids 4-24, 543-563, 624-644, 811-831

**N-glycosylation sites.**

amino acids 236-259, 370-373, 406-409, 413-416

**Tyrosine kinase phosphorylation sites.**

amino acids 35-41, 662-667

**N-myristoylation sites.**amino acids 17-22, 21-26, 134-140, 181-186, 254-259, 287-292, 355-360,  
405-410, 472-477, 593-598, 669-674, 746-751, 760-765, 764-769, 795-800,  
823-828**Amidation site.**

amino acids 365-368

**Ligand-gated ion channel.**

amino acids 543-834

**Receptor family ligand binding region.**

amino acids 56-398

150/162

**FIGURE 142**

MAITVPDGCERNGLKSKYYRLCDKEAANGCIVLETVTATAGVVTSVAFMLTLPILVCKVQDSRRRKMLETQFLFLG  
VIGIFGLTFPAFLIGLDGSTGSTRFFLFGILFSCICFSCLLAHAVSITKLVRGKKPLSLVILGLAVGFSLVQDVI  
AIEYIVLTWNTNVMVFSELSAPRANEUEVLLLTYYVILFMAITFLMSSFTFCGSGFTGWKRGAGHIYLTMLLSIA  
INVAWITLMLHPDFORWDDTILSSALAANGWVFLAYVSPEFWLLTKQRNPMDYFVEDAFCKFQLVKKSYGVE  
NRAYSQSEHTYQGFEETGDTLYAEYSTHFLQNGQFPQKEFSIPRAHAMPSTYKDYEVKKEGS

**Transmembrane domains.**

amino acids 30-59, 66-86, 98-118, 121-141, 137-157, 174-194, 212-232, 244-264

**N-glycosylation site.**

amino acids 158-161

**N-myristoylation sites.**

amino acids 8-13, 38-43, 80-85, 88-93, 102-107, 136-141, 201-206

**Amidation site.**

amino acids 124-127

**7 transmembrane receptor.**

amino acids 27-273

151/162

**FIGURE 143**

MLPAQEAARKLYSTNYVRNSRAIGVLWAIPTTICFAIVNVVCFIQPYWIGDGVDTFQSGYFGLFHYCIGNGFESREL  
TCPGSGFTDFSTLPSGAFKAASFEEIGLSMMLLIACLICFTLFFPCNTATVYKICAMMQLTSAAQIVLGCMIFPUG  
WDSUEVKRMCGEKTOKYTLGACSVRWAYILAIGILDALILSLFATVIGNRQDSLMAEELKAEKVLISQY9LE

**Transmembrane domains.**

amino acids 21-41, 93-113, 127-147, 173-193

**N-myristoylation sites.**

amino acids 23-28, 67-72, 89-94, 182-187

152/162

**FIGURE 144**

MPGAAAAAAAAAAMLPQGEAAKLYHTRYVNSRAIGVIAIETICFAIVNVVCFIQPYWIGDSVOTPQAGYFG  
LPHICTIGNGFSRELTGRGSFTDFSTLPSGAFKRAASFFTGLEMMLLIACILCFTLFFFTATVYKICAWMQLTS  
AAQLVLGCMIFPDGWUSDEVKRMCGEKTDRYTLGACSVRWAYILAIIGILDALILBFLAFVLGNBQDSIMAREL  
KAENKVLISQYSLE

**Transmembrane domains.**

amino acids 1-15, 34-54, 107-127, 141-161, 187-207

**N-myristoylation sites.**

amino acids 3-8, 37-42, 81-86, 103-108, 196-201



153/162

**FIGURE 145**

MFGAAAAAAAAAAMLPAGEAAKLYHTNYVRNSRAIGVLMATFTICPAIVNVVCFIQFYWTIGDGVDTTPQAGYFG  
LPHYCIGNGFSRELTCPGSPDPTLPSGAPKAASFTTGLSMMLIACILCFTLFFFPONTATVYFICAWMQLTG  
AACILVLGCMIEFDGWDSDDEVKRMCGEKTDKVTIGACSVRWAYILAIIGILDALILSFLAFVLGNRQDSLMBEEL  
KAENKYLSSQYSLE

**Transmembrane domains.**

amino acids 1-15, 34-54, 107-127, 141-161, 187-207

**N-myristoylation sites.**

amino acids 3-8, 37-42, 81-86, 103-108, 196-201

154/162

**FIGURE 146**

KFRLPCPCPRAGTYSSSESLGHPAPGQVTNRSPQEFMELFQSSRPPLQPVCTVCPGLELCPHRLAFSMAG  
LFSVVGTELLPLGLAALVQDNWLLQGLGALMSGLLLLFWGFPALFFESPFWLLATGQVARARKILWRFAESGVG  
FGDSSLGENSLATLMTLSARSQPRYH9PLGLLRVTWRNGLIGFSSLYGGIRASFRSLAPQVTTYLF  
YFLEAGLEAAALVFLLLTADCCGRFPVLLGTMTVGLASLLLLAGAQYLPCHTVLFLSVLGLASNAVSALSSL  
FAAEVFPTVIRGAGLGLVLGAGPLQAGPLDTLHGRQGFLLQVVFPASLAVLALLCVLLPFESRSGLPQSLQ  
DADELRRSPLLRCRPRQDHLPLPLPPSNYSWAGHTPEQH

**Transmembrane domains.**

amino acids 67-87, 102-122, 226-240, 249-269, 265-285, 301-321, 338-358

**Glycosaminoglycan attachment site.**

amino acids 145-148

**N-myristoylation sites.**

amino acids 14-19, 27-32, 57-62, 101-106, 145-151, 180-185, 191-196, 202-207,  
203-208, 228-233, 253-258, 283-288, 308-313, 312-317, 364-369

**Amidation site.**

amino acids 244-247

**Leucine zipper pattern.**

amino acids 96-117

**Sugar transport proteins.**

amino acids 117-126, 241-253, 276-321

155/162

**FIGURE 147**

MPEEQCHLSWKNVRPLYNAVSKELVGEFLQFVQLDKEASDFPDLNELDELSSKQKEELWQRLKMLITDVLLS  
 FVGGHQVVEAQGEDHMETEHGSKMKKSIELIYAITSVILASVSVINESENTAELECVITLMGLIYALPESERK  
 LQSSIQDLCVTEWKEGLPAKEUFGKTAFFVMLLRSLKLETKTGADVRLWRTHQALCFDYULEESGEIKDMLLEC  
 FININFIKKEEGRRFLSCLFNWMINFIKMINGTIRNQLQGLQKSLMVYIAEIZYFRANKKASGKILEATEMUCTQ  
 DFMFHGIALPRSPVHSKVKREVLSTPHRQKKVRQGVREMLYRLYKPIWRLGLKANNSEVSNAAALLFVSAFFIR  
 DPNLHAIBMSXIQQFEELYSLLEDPYPMVRSTGILGVCKITSKYWEMMPPFTLLIDLLKKVYTGELAFDTSSAD  
 VRCSVFKCLPMILDNKLSHPLLEQLLPALRYSLDNSEKVRVAFDMLLKIKAVRAAKFWKICPMRHILVRLET  
 DSRFVSRRLLSLIFMSFLPNQPEEVNCEECVTLVQMNHAAARRFYQYAHETACTNIAKLIHVIRHCLNACTQ  
 RAVREPPEDDEEDGKEKENVTLVDLTLGVNDVACMGALLEIIVILMKSIDRSMENNKSEKLYTINKFASVLPZ  
 YLKVFKDDRCKIPFLMLSMFPASAVPPFSCGVISTLSRSEGAVKRSYCTLLDCLCSWQGVGHILELVDNWL  
 TEHAQAKSNTASKGRVQIHOTRFVKEPELALVYIEYLLTHPKNRECLLSAFKKILNRLKALETSKADLESLLQT  
 FGGKPRGFSEAAAPRAFGLKRLSLRLQSKPCSEGVYLSMLEDTGSFWLESKILSFIQDQREEDYLKLHVIYQQ  
 ITQTLYLTCGDVVMVGLGDHQFMQLQRSLGIMQTVKGFVYVLLLDILKEITGSSLIQKTDSDDEEVAMLLDT  
 VQKVFQRMLECIARSERKQPEEGLALLYSVQRLHEFITAVQSRATDTPVHRGVLSFLTAGFVVEISHQLPKVS  
 DVEELTFPEHLSLDPFSPRLIGILIKSSNVVRSFLDELKACVASNDIEGIVCLTAAVHILVINAGKRRKSKV  
 RYVAATVHRKLKTFMEITLEEDSISRFLEYSSSRILGMLINS

**Transmembrane domain.**

amino acids 1081-1101

**N-glycosylation sites.**

amino acids 120-123, 612-615

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 280-283, 430-433, 1033-1036

**Tyrosine kinase phosphorylation sites.**

amino acids 99-106, 314-321, 329-337, 385-391, 844-852

**N-myristoylation sites.**

amino acids 137-142, 189-194, 254-259, 262-267, 698-703, 920-925, 1015-1020

**Amidation site.**

amino acids 233-236

**ATP/GTP-binding site motif A (P-loop).**

amino acids 167-174

**Leucine zipper pattern.**

amino acids 128-149, 135-156, 787-808

**Mitochondrial energy transfer proteins signature.**

amino acids 982-990

156/162

**FIGURE 148**

MEERETFFQAVSKELVGEFLQFVQLDKEASDPFSINELLDELRRKQKEELWQRLKNLLTDVILLESFVQGWQVVE  
 AQGEENMATERGSKRKSTIELIYAITSVILASVSVINESENVEALLECVIILNGILYALPESERKIQSSIQDLC  
 VTWKEGKGLYAKEDTGKTAFFVLLRRSLKETGTGADVCLRWIRIQRLYCFDYOLEESGGEIKDMLLECFININYKK  
 EECRRFLSCLFNWNNINTFKMIGTIKNQLQGLQKSLMVYIAEIIYFRWKKASGKILEAIENDCIQDEMFHGTNL  
 PRASPVHSKRVRELSYFHQKKVRQGVVEMLYRLYNPILMRGLKARNSEKRSNAALLEVSFAFYTRDPNLHATEM  
 DSKIQQKQPEELYSLLLEFPYPMVRSTGILGVCKITSKYWNEMMPPTILIDLKRVTEGELAFVTSSADVRCVSFRCCL  
 FMILDNKLSHPLEQLLPAIRYSLHDNSEKVRVAFVDMILKIKAVRAAKFWKICFNEHILVRLTDBRRPVSRRL  
 VSLIFNSFLPVNQPEEVCERCVTLVQMNHAAARRFYQYAHENTACTNIAKLEHVIRECLNACTQRAVREPPED  
 EEEEDGRENENVTVLDKTILSVNDVACMAGLLEIIVILWKSIDRSMMENKAKLYTINKPASVLFYILKVKEDDR  
 CRIPLFMLGFMPPASAVFPFSCGVISTLSREGEADVKSCTLLDCLCSWGQVGHILELVDMWLPTEHAQAKSN  
 TASKGRVQIHUTFPVKPELALVYIBYLLTHPKNPECLLSAPRKKLNHLKALETSHADLESLLQTPGGRPRGVS  
 EAAAPRAFGHLCRLSIHLQHKFCSEGVYLSMLEDTGFWLESKILSFIQDQEEDYLKLHVIYQQILQTYLTVFC  
 KDVVVVLGLDQFQMQQLQPSLGINQTVKGFYVSLLLDILKEITGSSLIQKTDSDDEEVAMLLDTVQKVFQKML  
 ECIAERSPKKQPEEGRLRLYGVQRPLHEFTTAVQSNHTDTPVHRGVLSLTIAGFVVEISGHLAKVSDVEELTPE  
 HSLDLPFPFRCLIGITIKSSNVRSFLDELKACVASNDTEGIVCLTAHVHLLVINAGKHKSSKVRVAVATVRR  
 KIKTFMETTLEEDSIERFLIESSSETLGEILLNS

**Transmembrane domain.**

amino acids 1072-1092

**N-glycosylation sites.**

amino acids 111-114, 603-606

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 3-6, 271-274, 421-424, 1024-1027

**Tyrosine kinase phosphorylation site.**

amino acids 91-97, 305-312, 320-328, 376-382, 835-843

**N-myristoylation sites.**

amino acids 128-133, 180-185, 245-250, 253-258, 689-694, 911-916, 1006-1011

**Amidation site.**

amino acids 224-227

**ATP/GTP-binding site motif A (P-loop).**

amino acids 158-165

**Leucine zipper pattern.**

amino acids 119-140, 126-147, 778-799

**Mitochondrial energy transfer proteins signature.**

amino acids 973-981

157/162

**FIGURE 149**

MNSTLFSQVENHSVHSNFSSENAQLAFENDDCHLPLAMIFTLALAYQAVLLIGVSGNIALLLIILKQKEMRNV  
TNILIVNLSFSDELVAIMCLPFTFVYTLMDHNWVFGAMCKLNFFVQCVSITVSIFSLVLLAVERHQILIINERGW  
RPNNRHAYVGTIAVITWVLAVASSLPFLIYQVMTDEPFQNVTLDAYKDKIVCTDQFFSDSHPLSYITLLLVLYFG  
PLCFIFICYFKIVITRLRRNNMMENMRDNHYPSSETKRINIMLLSIVVAFAVCMLPLTIFNTFVFDWNAQIYATC  
NHNLLPLACHLTANISTCVNPIFYGFLNKNFORDLQFTTNFCDFRSRDDDYETIAMSTMHTDVSKTSLKQASPV  
AFKKINNNDDNEKI

**Transmembrane domains.**

amino acids 38-58, 78-98, 117-137, 155-175, 208-228, 260-280, 296-316

**N-glycosylation sites.**

amino acids 2-5, 11-14, 17-20, 73-76, 81-84, 186-189

**Tyrosine kinase phosphorylation sites.**

amino acids 247-253, 341-347

**N-myristoylation site.**

amino acids 54-59

**7 transmembrane receptor (rhodopsin family).**

amino acids 57-320

158/162

**FIGURE 150**

MVRCDRGLQMLLTTAGAAFAAFSLMAIAIGTDYWLXSSAHICNGSTNLTMDUGPPFRKAGDLTHSGLNREVCCEG  
IYKGHCFRIMHFFEDNDYDHDSSYYLLRIVRASSVFFILSTIELLLGGLCIGAGRIYSRKNNIVLSAGILFVAA  
GLSNIGITIIYIISSTGDPDSKRDCKKNHYNFGWSTFFGALSFIVAEIVGLAVNIYIEKKELRFKTEREPL  
KASSSSPYARMPSTPYRRRRSRSSSRSTEASPSRUVSPMGLKITGAIPMGELSMYILSRFLKVFTTAAAGYSPDQ  
EASFLOQVHDFQQDLKEGFRVSMILNRRTTPV

**Signal sequence.**

amino acids 1-19

**Transmembrane domains.**

amino acids 103-123, 140-160, 192-202

**N-glycosylation sites.**

amino acids 42-45, 45-48

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 240-243, 322-325

**N-myristoylation sites.**

amino acids 16-21, 43-48, 74-79, 122-127, 262-267

**Cell attachment sequence.**

amino acids 58-60

**FMP-22/EMF/MP20/Claudin family.**

amino acids 6-202

159/162

**FIGURE 151**

MARGPGLAPPPRLRLLELLLVLAAVTGHATAQDSCTCPTNEMTVCSFDGPGGRCCQCRALGSGMAVDCSTLTSTKCL  
LLKAPMSAPKNARTLVRPSEHALVDNDGLYDFDCDFEGRFKARQCNTSVWCVCVNSVGVRRTKGGLSLECDLL  
VTHNTLTDLREKPTAGAFNNSDLDAELRLFRERYRLRPFVAAVHYEQFTIQLELRQATSQKARGVDLGDA  
AYYFERDINGESLFGGRGGLGLVVGEPLOVERTLIYYLDEIPEKFSMKPLTAGLIAVIVVVVALVAGMAVLV  
ITNRRKSGYKKVLEIKELGELAKEPSL

**Signal sequence.**

amino acids 1-26

**Transmembrane domain.**

amino acids 274-294

**N-glycosylation sites.**

amino acids 33-36, 120-123, 160-171, 200-211

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 271-274, 300-303

**N-myristoylation sites.**

amino acids 59-64, 132-137

**Thyroglobulin type-1 repeat.**

amino acids 73-145

160/162

**FIGURE 152**

MGKCSGRCTLVAFCCQLVAAERQIFDFESYQWAPILANFLAIMAVILGIFGTVQYRSRYLLYRAHIVLVVG  
WNAFIICFYLEVGGQLSQDRDFIMTENTSLHRSWMMENGPGCLVTPVINSRLALEDHHEVISVTGCLLDYFYIEAL  
GSALQIFLALFGFVFACYVSKVPLEEDSFDFLGGFDSYGYQAPQKTSHLQLQPLYTSG

Signal sequence.

amino acids 1-21

Transmembrane domains.

amino acids 33-53, 62-82, 147-167

N-glycosylation site.

amino acids 100-103

Tyrosine kinase phosphorylation site.

amino acids 24-32

N-myristoylation sites.

amino acids 50-55, 182-187



161/162

**FIGURE 153**

MPAPRAREQPRVPGERQPLLPRGARQPRRWKRAAGAAVLLVEMLERAAFFGVNTANLVLYLMSTNFNWTGSEQATH  
 AALVFLGASYLLAPVGGWLDVYLGRYRAVALSLLLYLAASGLLPATAFPDGRSSFCGEMTASPLGPACPSAGC  
 PRSSPSPYCAPVLYAGLLLLGLAASSVRSNLTSPGADQVNDLGRDATERFTFNWYWSINLGAVLBSLLVVAFIQQ  
 NISFLLGYSIPVGCVGLAFFIFLPATPVFFITKPPMGSQVSSMLKLALQNCPPQLWQRHSARLRQCARVLADEES  
 PQGASPFQEDIANEQVYVKILPVMYTLVFYMMVYFQMNSTYVLQGLHLHLPNIFPEANFANISVALRAQGSSTYI  
 FRAWLLANVVVVLILNPLKDRLLDPLLECKLLPSALQKMLGMFFGFTSVIVAGVLEMERLHYIEHNETVSG  
 QTGEVLYNAAPLSTWQIPQYLLIGISHIFASIFGLEEFAYSEAPRSMQGAIMGITFFCLSGVSGELGSSLVALLS  
 LFGGWLRCPKDFGINNNCRMDLYFFLAGIQAVTALLPVWLAGRYERRASQGPASHSRFSRNG

**Transmembrane domains.**

amino acids 35-55, 73-93, 98-118, 157-177, 199-219, 250-270, 341-361,  
 369-389, 408-428, 457-477, 499-519, 537-557

**N-glycosylation sites.**

amino acids 61-64, 66-69, 178-181, 223-226, 356-359, 439-442

**Glycosaminoglycan attachment site.**

amino acids 503-506

**N-myristoylation sites.**

amino acids 51-56, 90-95, 116-121, 147-152, 169-174, 209-214, 258-263,  
 365-370, 414-419, 479-484, 493-498, 497-502, 506-511, 531-536

**POT family.**

amino acids 101-503

162/162

**FIGURE 154**

MWVNPPEVILANADWITERANPYFILQRRKHAGDGGGGGLAGLVGTLDVVLDSSARVAPYRIIVQTPDLSLV  
 YWTLACGGSRKEITEHSEWLEQNLLQFLSIFENENDITTFVPGKIQGILAEYNKINDVKEDDDTEKFKERIVKF  
 GRIFGMPPEEKLYVHYISCSYWKSKVPRKQWMLSYNBLCFYSFLMGREAKLVIRWVDITQLERWATLLLPDVIK  
 VSTRSEHFTSVFLININETFKLMEQLANIAMRQLLUNEGFEQORSIFMLKRKSPKKVSLEPQLDARKKSERYR  
 ALERLPKDEKLDGHTDCLTWTPFNKMHILQGMVFSTNIOFTSKEENLCSLITVLPVEVITVEKADSSSVLPSPFL  
 SISTRNMTFLFANLKDRDFLVQPRISDFLQQTESKLYSDKEFAGSYNGSDDEVYGRSPSSLVSSSPQRSTSSDAD  
 GERQFNLMNGNSVPEMTQITMTMYRRRSPEEFNPKLAKETFKQAWKHIEAEGQGICMYRTERTRELVLKGIPE  
 SMRGLJWLLLSGAINERATHEGYEDELVEKSMCKNYHLATEETIERDLHRSLEPEHAFQRENGIAALRRVLTAXAF  
 RNFNIGYQARMNIVTSVLLLYAREEEAFWLLVALCERMLPDYINTRVVGAALVQGVFEELARDYVPQLYDCMQD  
 LGVISTISLSWFLTLFLSVMPFESAVVVVDCEFFYSGIRVIFQLALAVLDANVDKLLNCKDDGHEMTVLGRYLES  
 VTNKDSFTFPIPLHSLSDDDVEPYPEVDIFRLIRTSYEKEGTTRADLIEQMRFKQRLKVIQTLDDTTKRNVR  
 TIVTETFTIDELEKLYALFRAEHLTSCYWGSSNALDRHDPSELPYLEQYRIDFEQEGMFALLFWACGTHSD  
 VLASRLFQLLDENGDSLLNFRFVSGLSAACHGDLTEKLLKLYRMVLPFEPSSDQDEPQSAFETATQVFFEDYTF  
 ECTHVVLGDSRSFQADDGPVTVSLKPKDKGRANSQENRMYLRLWTFENKSKSGKAKDLPEKLNQQGFTELCKTH  
 YNMFSEDFNEQLVYATAAFTVSLLEIGEVGKLFVAQPAKEGGSGGSGPSCHQGTPGVLPFKKPGQPYVVSFV  
 EPLPASLAPDSEENSLGCGMEUTKLEDDSPRNGACSSMLISDDDTKDDSSMSYSVLSAGSHEDKLHCEIG  
 EDTVLVRSQGQTAALPRSTSLDRDWAITFEQFLASLLTEPALVKYFDKPVCMARITSAKNIRNMKGKPLTSASD  
 YELSAMSG

**Transmembrane domains.**

amino acids 35-55, 669-689

**N-glycosylation sites.**

amino acids 212-215, 239-242, 417-420, 1011-1014

**Glycosaminoglycan attachment site.**

amino acids 1192-1195

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 272-275, 277-280, 468-471

**N-myristoylation sites.**

amino acids 36-41, 37-42, 39-44, 40-45, 44-49, 414-419, 497-502, 515-520,  
 668-673, 782-787, 845-850, 846-851, 914-919, 977-982, 1078-1083, 1079-1084,  
 1082-1087, 1144-1149, 1193-1198

**Amidation site.**

amino acids 991-994

**TBC domain.**

amino acids 512-724

**S-100/ICaBP type calcium.**

amino acids 891-911

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/19592

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07K 16/18, 16/30; G01N 33/574  
US CL : 530/300, 330, 387.7, 387.9, 387.3, 395; 424/130.1, 133.1, 141.1, 155.1; 435/172.2, 328, 344, 330, 7.  
According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/300, 330, 387.7, 387.9, 387.3, 395; 424/130.1, 133.1, 141.1, 155.1; 435/172.2, 328, 344, 330

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
WEST, GenCore databases

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,965,710 A (BODMER et al) 12 October 1999 (12.10.1999), column 9, lines 14-19; column 10, lines 10-11; Example 6 of columns 17-19; Sequence 34 within columns 49-52 and attached database sheet.	1-9 and 12-15
Y	US 4,351,598 A (HASEGAWA et al) 25 May 1982 (25.05.1982), abstract, column 16, lines 65-68.	10 and 11

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

### \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "B" earlier applications or patents published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"X" prior documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principles or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"Z" document member of the same patent family

Date of the actual completion of the international search

26 May 2003 (26.05.2003)

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, Virginia 22313-1450

Facsimile No. (703)305-3230

Date of mailing of the international search report

04 JUN 2003

Authorized officer

Alana M. Harris, Ph.D.

Telephone No. (703)308-0196